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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM																								
(57) Abstract Novel polynucleotides and the proteins encoded thereby are disclosed.																								

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SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone bn365_53 deposited under accession number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone bn365_53 deposited under accession number ATCC 98752;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:2;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366; the nucleotide sequence of the full-length

5 SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

This application is a continuation-in-part of the following applications:

- 10 (1) provisional application Ser. No. 60/084,564, filed May 7, 1998;
 (2) provisional application Ser. No. 60/087,645, filed June 2, 1998;
 (3) provisional application Ser. No. 60/093,712, filed July 22, 1998;
 (4) provisional application Ser. No. 60/094,935, filed July 31, 1998;
 (5) provisional application Ser. No. 60/095,880, filed August 10, 1998;
 (6) provisional application Ser. No. 60/096,068, filed August 11, 1998;
15 all of which are incorporated by reference herein.

FIELD OF THE INVENTION

20 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

25 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by
35 virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

protein coding sequence of clone bn365_53 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bn365_53 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
20 consisting of:

(aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
15 cDNA sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:3 from nucleotide 1358 to nucleotide 1915;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone bo342_2 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915; the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915; the nucleotide sequence of the full-length protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and
 - (ab) the nucleotide sequence of the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:4 having biological activity, the fragment comprising the amino acid sequence from
10 amino acid 280 to amino acid 289 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;

15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn721_8 deposited under accession number ATCC 98752;

20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn721_8 deposited under accession number ATCC 98752;

25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

30 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689; the nucleotide sequence of the full-length
10 protein coding sequence of clone dn721_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn721_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending
20 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, and extending
25 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred
5 -- embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from
10 amino acid 318 to amino acid 327 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- 20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn834_1 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone dn834_1 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484; the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892; the nucleotide sequence of the full-length protein coding sequence of clone dn834_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn834_1 deposited
15 under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

15 (bb) the nucleotide sequence of the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated
25 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 20 to
30 nucleotide 484. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide

18 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420; the nucleotide sequence of the full-length protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752. In further preferred
20 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having
25 biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, and extending

contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 98 to amino acid 107 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:11 from nucleotide 918 to nucleotide 1295;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe80_1 deposited under accession number ATCC 98752;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe80_1 deposited under accession number ATCC 98752;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone pe80_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pe80_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having

biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428; the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35
5 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 pm113_1 deposited under accession number ATCC 98752;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496;

5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm749_8 deposited under accession number ATCC 98752;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;

10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm749_8 deposited under accession number ATCC 98752;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;

15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496; the nucleotide sequence of the full-length protein coding sequence of clone pm749_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm749_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

of clone pm749_8 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide
15 108 to nucleotide 1496.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such
25 protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ
30 ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;

5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752;

10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752;

15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023; the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023; the nucleotide sequence of the full-length protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752; or the

nucleotide sequence of a mature protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

- (bb) the nucleotide sequence of the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv296_5 deposited under accession number ATCC 98752;

15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv296_5 deposited under accession number ATCC 98752;

20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299; the nucleotide sequence of the full-length protein coding sequence of clone pv296_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pv296_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;

10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er311_20 deposited under accession number ATCC 98781;

15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er311_20 deposited under accession number ATCC 98781;

20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008; the nucleotide sequence of the full-length protein coding sequence of clone er311_20 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone er311_20 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(ab) the nucleotide sequence of the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;

10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;

15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;

20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043; the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043; the nucleotide sequence of the full-length protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and
 - (ab) the nucleotide sequence of the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;

- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099; the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide

47 to nucleotide 1099. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
 - (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl87_1 deposited under accession number ATCC 98781;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl87_1 deposited under accession number ATCC 98781;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259; the nucleotide sequence of the full-length protein coding sequence of clone pl87_1 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pl87_1 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:28;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm514_4 deposited under accession
30 number ATCC 98781;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm514_4 deposited under accession number ATCC 98781;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284; the nucleotide sequence of the full-length protein coding sequence of clone pm514_4 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pm514_4 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co155_12 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co155_12 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997; the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997; the nucleotide sequence of the full-length protein coding sequence of clone co155_12 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone co155_12 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having

biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343; the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343; the nucleotide sequence of the full-length protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide
15 21 to nucleotide 1343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of
20 said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such
30 protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:35 from nucleotide 235 to nucleotide 899;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lv2_47 deposited under accession number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lv2_47 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone lv2_47 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:36;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557; the nucleotide sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone lv2_47 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone lv2_47 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
 - (ab) the nucleotide sequence of the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide
20 557, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
25 NO:35 from nucleotide 235 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;

(c) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(d) the amino acid sequence encoded by the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36 or the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an
15 isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499; the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499; the nucleotide sequence of the full-length protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide

104 to nucleotide 499. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from
5 nucleotide 215 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:38;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm96_9 deposited under accession
30 number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm96_9 deposited under accession number ATCC 98808;

5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:39.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861; the nucleotide sequence of the full-length protein coding sequence of clone pm96_9 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pm96_9 deposited under accession number ATCC 98808. In other preferred embodiments, the
25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
30 preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762; the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having

biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the
3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone
pu261_1 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw214_15 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw214_15 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824; the nucleotide sequence of the full-length protein coding sequence of clone pw214_15 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pw214_15 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having
5 biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

30 (bb) the nucleotide sequence of the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qb56_19 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qb56_19 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone qb56_19 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qb56_19 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

15 (ab) the nucleotide sequence of the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273; the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273; the nucleotide sequence of the full-length protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

- (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

- (ab) the nucleotide sequence of the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

- (bb) the nucleotide sequence of the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide
10 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:47 from nucleotide 242 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf116_2 deposited under accession number ATCC 98808;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf116_2 deposited under accession number ATCC 98808;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097; the nucleotide sequence of the full-length protein coding sequence of clone qf116_2 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf116_2

deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808. In further preferred
5 comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147
10 to amino acid 156 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

- (bb) the nucleotide sequence of the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;

5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;

10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;

15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;

20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741; the nucleotide sequence of SEQ ID NO:51

from nucleotide 595 to nucleotide 741; the nucleotide sequence of the full-length protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am748_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am748_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196; the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196; the nucleotide sequence of the full-length protein coding sequence of clone am748_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone am748_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj507_1 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj507_1 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:55.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310; the nucleotide sequence of the full-length protein coding sequence of clone cj507_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cj507_1 deposited under accession number ATCC 98817. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

- (ab) the nucleotide sequence of the cDNA insert of clone
cj507_1 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:55, but excluding the poly(A) tail at the
3' end of SEQ ID NO:55; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 cj507_1 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide
1310, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide
- 30 51 to nucleotide 1310.

In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the group
consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;

20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cn922_5 deposited under accession number ATCC 98817;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cn922_5 deposited under accession number ATCC 98817;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328; the nucleotide sequence of the full-length protein coding sequence of clone cn922_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cn922_5 deposited under accession number ATCC 98817. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

- (ab) the nucleotide sequence of the cDNA insert of clone
cn922_5 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:57, but excluding the poly(A) tail at the
3' end of SEQ ID NO:57; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 cn922_5 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide
1328, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide
- 30 195 to nucleotide 1328.

In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the group
consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;

- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw691_11 deposited under accession
- 20 number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone cw691_11 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:60;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone cw691_11 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw691_11 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

- (ab) the nucleotide sequence of the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 cw691_11 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide
- 30 76 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;

- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252; the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252; the nucleotide sequence of the full-length protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide

11 to nucleotide 1252. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from
5 nucleotide 119 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:62;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:63 from nucleotide 451 to nucleotide 1296;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296; the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296; the nucleotide sequence of the full-length protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having

biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the
3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone
cw1640_1 deposited under accession number ATCC 98817;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone d24_1 deposited under accession number ATCC 98817;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone d24_1 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827; the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827; the nucleotide sequence of the full-length protein coding sequence of clone d24_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone d24_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide

encodes the full-length or a mature protein encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide
15 66 to nucleotide 827. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of
20 said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such
30 protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;

 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;

10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529;

 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817;

15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;

 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817;

20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;

 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;

25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529; the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817; or the
5 nucleotide sequence of a mature protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817. In further preferred
10 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having
15 biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 58 to amino acid 67 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone di393_2 deposited under accession
20 number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone di393_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543; the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543; the nucleotide sequence of the full-length protein coding sequence of clone di393_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone di393_2 deposited
15 under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

- (ab) the nucleotide sequence of the cDNA insert of clone di393_2 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 di393_2 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide
- 30 31 to nucleotide 543. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from

nucleotide 88 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone
10 di393_2 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167_2 deposited under accession
25 number ATCC 98818;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167_2 deposited under accession number
30 ATCC 98818;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356; the nucleotide sequence of the full-length protein coding sequence of clone dj167_2 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dj167_2 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 dj167_2 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:73 from nucleotide 1485 to nucleotide 4490;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167_19 deposited under accession
30 number ATCC 207090;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167_19 deposited under accession number ATCC 207090;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343; the nucleotide sequence of the full-length protein coding sequence of clone dj167_19 deposited under accession number ATCC 207090; or the nucleotide sequence of a mature protein coding sequence of clone dj167_19 deposited under accession number ATCC 207090. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
5 corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490. Also preferably the polynucleotide isolated according to the
10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490. Also
15 preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, to a nucleotide sequence corresponding to the 3' end of said
20 sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- 25 (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
- (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (d) the amino acid sequence encoded by the cDNA insert of clone
30 dj167_19 deposited under accession number ATCC 207090;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74 or the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence
5 from amino acid 513 to amino acid 522 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw665_4 deposited under accession
15 number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
20 protein coding sequence of clone dw665_4 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:76;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441; the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441; the nucleotide sequence of the full-length protein coding sequence of clone dw665_4 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dw665_4 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592;

20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx146_12 deposited under accession number ATCC 98818;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx146_12 deposited under accession number ATCC 98818;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592; the nucleotide sequence of the full-length protein coding sequence of clone dx146_12 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx146_12 deposited under accession number ATCC 98818. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

- (ab) the nucleotide sequence of the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

- (bb) the nucleotide sequence of the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide
- 30 78 to nucleotide 1592.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;

- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:79 from nucleotide 337 to nucleotide 948;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone dx219_13 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948; the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948; the nucleotide sequence of the full-length protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide

19 to nucleotide 948. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from
5 nucleotide 337 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:80;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:81 from nucleotide 62 to nucleotide 286;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286; the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286; the nucleotide sequence of the full-length protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the

fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone h225_1 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone h225_1 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
30 NO:83 from nucleotide 141 to nucleotide 572; the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572; the nucleotide sequence of the full-length protein coding sequence of clone h225_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone h225_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide

encodes the full-length or a mature protein encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83; and

(bb) the nucleotide sequence of the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, and extending contiguously from a nucleotide sequence
10 corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
- (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210; the nucleotide sequence of SEQ ID NO:85

from nucleotide 505 to nucleotide 3210; the nucleotide sequence of the full-length protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:86;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and

(c) the amino acid sequence encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899; the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

10 (bb) the nucleotide sequence of the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from
30 nucleotide 522 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
5 ml236_5 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452; the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide

6 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from
5 nucleotide 399 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:91 from nucleotide 682 to nucleotide 1179;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone at94_2 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone at94_2 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179; the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179; the nucleotide sequence of the full-length protein coding sequence of clone at94_2 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone at94_2 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the

fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf169_13 deposited under accession number ATCC 98822;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf169_13 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077; the nucleotide sequence of the full-length protein coding sequence of clone bf169_13 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bf169_13 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

- (ab) the nucleotide sequence of the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

- (bb) the nucleotide sequence of the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bl152_12 deposited under accession number ATCC 98822;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bl152_12 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone bl152_12 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bl152_12 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

15 (ab) the nucleotide sequence of the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:96;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
bl152_12 deposited under accession number ATCC 98822;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bz578_1 deposited under accession number ATCC 98822;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bz578_1 deposited under accession number ATCC 98822;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816; the nucleotide sequence of the full-length protein coding sequence of clone bz578_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bz578_1 deposited under accession number ATCC 98822. In other preferred embodiments, the
30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

15 (ab) the nucleotide sequence of the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

(bb) the nucleotide sequence of the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:98;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992; the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992; the nucleotide sequence of the full-length protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

- (ab) the nucleotide sequence of the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;

- (ii) hybridizing said probe(s) to human genomic DNA in
20 conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:99, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:99; and

- (bb) the nucleotide sequence of the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;

- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide
10 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:99 from nucleotide 765 to nucleotide 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the
fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ch245_1 deposited under accession number ATCC 98822;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ch245_1 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480; the nucleotide sequence of the full-length protein coding sequence of clone ch245_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ch245_1

deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822. In further preferred
5 comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino
10 acid 45 to amino acid 54 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
- (ab) the nucleotide sequence of the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

- (bb) the nucleotide sequence of the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;

5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj378_3 deposited under accession number ATCC 98822;

10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj378_3 deposited under accession number ATCC 98822;

15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541; the nucleotide sequence of the full-length protein coding sequence of clone cj378_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cj378_3 deposited

under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
 - (ab) the nucleotide sequence of the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

- (bb) the nucleotide sequence of the cDNA insert of clone
cj378_3 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide
541, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide
281 to nucleotide 541.

In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the group
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the
fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 cj378_3 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred
embodiments, the present invention provides a protein comprising a fragment of the
amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:104 having biological activity, the fragment comprising the amino acid sequence
from amino acid 38 to amino acid 47 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;

5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;

10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1481_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;

15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1481_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;

20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202; the nucleotide sequence of SEQ ID

NO:105 from nucleotide 401 to nucleotide 2349; the nucleotide sequence of the full-length protein coding sequence of clone cw1481_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cw1481_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905; the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905; the nucleotide sequence of the full-length protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone df202_3 deposited under accession number ATCC 98822;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone df202_3 deposited under accession number ATCC 98822;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369; the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369; the nucleotide sequence of the full-length protein coding sequence of clone df202_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone df202_3 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide

16 to nucleotide 369. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from
5 nucleotide 103 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:110;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone km225_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone km225_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539; the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539; the nucleotide sequence of the full-length protein coding sequence of clone km225_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone km225_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112

having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the
3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone
km225_1 deposited under accession number ATCC 98822;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030; the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030; the nucleotide sequence of the full-length protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822. In other preferred

30

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113
15 from nucleotide 1734 to nucleotide 2030. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, to a nucleotide
20 sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:114;
(b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
(c) the amino acid sequence encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;
30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350; the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350; the nucleotide sequence of the full-length protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

(ab) the nucleotide sequence of the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

(bb) the nucleotide sequence of the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone my340_1 deposited under accession
- 20 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone my340_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:117.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094; the nucleotide sequence of the full-length protein coding sequence of clone my340_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone my340_1 deposited under accession number ATCC 98822. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

- (ab) the nucleotide sequence of the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 my340_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide
- 30 837 to nucleotide 1094.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial,
15 yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

20 (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and

(b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

25 Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically
30 effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

5 ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length
10 and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available
15 at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell
20 in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "bn365_53"

A polynucleotide of the present invention has been identified as clone "bn365_53".
25 bn365_53 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn365_53 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
30 as "bn365_53 protein").

The nucleotide sequence of bn365_53 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn365_53 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bn365_53 should be approximately 650 bp.

The nucleotide sequence disclosed herein for bn365_53 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn365_53 demonstrated at least some similarity with sequences identified as AA242967 (zr65g11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 668324 5') and N40141 (yw73c12.r1 Homo sapiens cDNA clone 257878 5'). The predicted amino acid sequence disclosed herein for bn365_53 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bn365_53 protein demonstrated at least some similarity to sequences identified as D63484 (KIAA0150 protein [Homo sapiens]) and to the GAGE-1 to GAGE-6 family of human proteins expressed in tumors (GenBank Accession Numbers U19142-U19147). The amino acid sequence of SEQ ID NO:2 contains two RGD (Arg-Gly-Asp) motifs (around residues 12 and 75): the sequence Arg-Gly-Asp, found in fibronectin, is crucial for its interaction with its cell surface receptor, an integrin. What has been called the 'RGD' tripeptide is also found in the sequences of a number of other proteins, where it has been shown to play a role in cell adhesion. These proteins are: some forms of collagens, fibrinogen, vitronectin, von Willebrand factor (VWF), snake disintegrins, and slime mold discoidins. Based upon sequence similarity, bn365_53 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bn365_53 indicates that it may contain one or more repetitive elements.

Clone "bo342_2"

A polynucleotide of the present invention has been identified as clone "bo342_2". bo342_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo342_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bo342_2 protein").

The nucleotide sequence of bo342_2 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo342_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino

acids 372 to 384 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 385. Amino acids 1 to 13 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 14. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the bo342_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo342_2 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for bo342_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bo342_2 demonstrated at least some similarity with sequences identified as AA306000 (EST177027 Jurkat T-cells VI Homo sapiens cDNA 5' end) and W94256 (ze12b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358731 3' similar to contains Alu repetitive element). Based upon sequence similarity, bo342_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the bo342_2 protein sequence, centered around amino acids 300, 320, 380, 410, 430, and 490 of SEQ ID NO:4, respectively. The nucleotide sequence of bo342_2 indicates that it may contain Alu or other repetitive elements.

Clone "dn721_8"

A polynucleotide of the present invention has been identified as clone "dn721_8". dn721_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn721_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn721_8 protein").

The nucleotide sequence of dn721_8 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn721_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn721_8 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for dn721_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn721_8 demonstrated at least some similarity with sequences identified as H63637 (yr34b12.r1 Homo sapiens cDNA clone 207167 5'), N31598 (yy20b12.s1 Homo sapiens cDNA clone 271775 3'), and R61419 (yh15e05.r1 Homo sapiens cDNA clone 37671 5'). Based upon sequence similarity, dn721_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the dn721_8 protein sequence, one centered around amino acid 269 and another around amino acid 457 of SEQ ID NO:6.

Clone "dn834_1"

A polynucleotide of the present invention has been identified as clone "dn834_1". dn834_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn834_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn834_1 protein").

The nucleotide sequence of dn834_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn834_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn834_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for dn834_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn834_1 demonstrated at least some similarity with sequences identified as AA544005 (vj83h07.r1 Soares mouse mammary gland NbMMG Mu's musculus cDNA clone 935677 5'), AL022163 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 551E13; HTGS phase 1), L44560 (Homo sapiens thymus mRNA (randomly primed, normalized), single-pass sequence), and T72271 (Human B cell surface antigen cDNA). The predicted amino acid sequence disclosed herein for dn834_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted dn834_1 protein demonstrated at least some similarity to sequences identified as R47496 (Translated sequence of domains I and II of celD cDNA in clone pCNP4). Based upon sequence similarity, dn834_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
5 program predicts three potential transmembrane domains within the dn834_1 protein sequence, centered around amino acids 59, 84, and 145 of SEQ ID NO:8, respectively.

dn834_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

10

Clone "pd278_5"

A polynucleotide of the present invention has been identified as clone "pd278_5". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods
15 which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate pd278_5 from a human adult kidney cDNA library. pd278_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to
20 herein as "pd278_5 protein").

The nucleotide sequence of pd278_5 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pd278_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino
25 acids 61 to 73 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 74. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pd278_5 protein.

30 There are two additional and mutually overlapping possible open reading frames close to the 5' end of SEQ ID NO:9 (bases 82 - 420 and bases 119 - 414). The translated open reading frame of bases 119 - 414 has a predicted leader/signal sequence from amino acid 49 to amino acid 61, with the predicted mature amino acid sequence beginning at

amino acid 62. Each of the additional possible open reading frames has a predicted transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pd278_5 should be approximately 2000 bp.

5 The nucleotide sequence disclosed herein for pd278_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pd278_5 demonstrated at least some similarity with sequences identified as AA292241 (zt50d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725781 5'), AA428245 zw51d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens
10 cDNA clone 773587 3'), AA599487 (ag23f05.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071201 3'), AA827135 (ob53b03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1335053 3'), H54322 (yq90d03.s1 Homo sapiens cDNA clone 203045 3'), and T22170 (Human gene signature HUMGS03741). The predicted amino acid sequence disclosed herein for pd278_5 was searched against the GenPept and GeneSeq amino acid
15 sequence databases using the BLASTX search protocol. The predicted pd278_5 protein demonstrated at least some similarity to sequences identified as R13144 (Deleted in Colorectal Carcinomas) and X13885 (extensin (AA 1-620) [Nicotiana tabacum]). Based upon sequence similarity, pd278_5 proteins and each similar protein or peptide may share at least some activity.

20

Clone "pe80_1"

A polynucleotide of the present invention has been identified as clone "pe80_1". pe80_1 was isolated from a human adult blood (chronic myelogenous leukemia K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins
25 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe80_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe80_1 protein").

The nucleotide sequence of pe80_1 as presently determined is reported in SEQ ID
30 NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe80_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe80_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pe80_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe80_1 demonstrated at least some similarity with sequences identified as AA291078 (zs47b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
5 IMAGE:700591 5'), AA429912 (zw66e06.s1 Soares testis NHT Homo sapiens cDNA clone 781186 3'), H82367 (yv79d06.r1 Homo sapiens cDNA clone 248939 5' similar to contains Alu repetitive element;contains OFR repetitive element), Q60627 (Human brain Expressed Sequence Tag EST02640), and R20261 (yg20a02.r1 Homo sapiens cDNA clone 32587 5').
10 Based upon sequence similarity, pe80_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the pe80_1 protein sequence, one centered around amino acid 58 and another around amino acid 109 of SEQ ID NO:12. The nucleotide sequence of pe80_1 indicates that it may contain an Alu repetitive element.

15 Clone "pm113_1"

A polynucleotide of the present invention has been identified as clone "pm113_1". pm113_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
20 of computer analysis of the amino acid sequence of the encoded protein. pm113_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm113_1 protein").

The nucleotide sequence of pm113_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the pm113_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 41 to 53 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
30 should the predicted leader/signal sequence not be separated from the remainder of the pm113_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm113_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for pm113_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm113_1 demonstrated at least some similarity with sequences identified as AA009482 (zi04c03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429796 5'), AA350890 (EST58401 Infant brain Homo sapiens cDNA 3' end), AC003030 (Human DNA from chromosome 19-specific cosmid R29828, genomic sequence, complete sequence), H98961 (yx11b02.s1 Homo sapiens cDNA clone 261387 3'), R07796 (yf15e05.r1 Homo sapiens cDNA clone), T22151 (Human gene signature HUMGS03721), and W68491 (zd34h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342579 5'). Based upon sequence similarity, pm113_1 proteins and each similar protein or peptide may share at least some activity.

Clone "pm749_8"

A polynucleotide of the present invention has been identified as clone "pm749_8". pm749_8 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm749_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm749_8 protein").

The nucleotide sequence of pm749_8 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm749_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm749_8 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pm749_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm749_8 demonstrated at least some similarity with sequences identified as AA314025 (EST185879 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end) and AA374458 (EST86612 HSC172 cells I Homo sapiens cDNA 5' end). The predicted amino acid sequence disclosed herein for pm749_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted pm749_8 protein demonstrated at least some similarity to sequences identified as D89169 (similar to *Saccharomyces cerevisiae* SCD6 protein, SWISS-PROT Accession Number P45978 [*Schizosaccharomyces pombe*]) and U30384 (Scd6p [*Saccharomyces cerevisiae*]). Based upon sequence similarity, pm749_8 proteins and each
5 similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm749_8 protein sequence centered around amino acid 138 of SEQ ID NO:16.

Clone "pt31_4"

10 A polynucleotide of the present invention has been identified as clone "pt31_4". pt31_4 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pt31_4
15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt31_4 protein").

The nucleotide sequence of pt31_4 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt31_4 protein corresponding
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 19 to 31 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt31_4
25 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt31_4 should be approximately 3200 bp.

The nucleotide sequence disclosed herein for pt31_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. pt31_4 demonstrated at least some similarity with sequences identified as AA348130 (EST54532 Fetal heart II *Homo sapiens* cDNA 5' end), AA350691 (EST58082 Infant brain *Homo sapiens* cDNA 5' end), AC001226 (Genomic sequence from Human 13, complete sequence), H22773 (ym54c06.r1 *Homo sapiens* cDNA clone 52351 5'), and R21869 (yh22b10.s1 *Homo sapiens* cDNA clone 130459 3'). The predicted amino

acid sequence disclosed herein for pt31_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pt31_4 protein demonstrated at least some similarity to sequences identified as U53147 (C01B7.6 [Caenorhabditis elegans]). Based upon sequence similarity, pt31_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the pt31_4 protein sequence, centered around amino acids 90, 110, 210, 410, and 590 of SEQ ID NO:18, respectively.

10 Clone "pv296_5"

A polynucleotide of the present invention has been identified as clone "pv296_5". pv296_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv296_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv296_5 protein").

The nucleotide sequence of pv296_5 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv296_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv296_5 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pv296_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv296_5 demonstrated at least some similarity with sequences identified as AA022471 (ze70c01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364320 3'), AA335246 (EST39647 Epididymus Homo sapiens cDNA 5' end), and AA481308 (zv06a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752816 5'). Based upon sequence similarity, pv296_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv296_5 protein sequence centered around amino acid 32 of SEQ ID NO:20.

Clone "er311_20"

A polynucleotide of the present invention has been identified as clone "er311_20". er311_20 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. er311_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "er311_20 protein").

The nucleotide sequence of er311_20 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the er311_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 654 to 666 of SEQ ID NO:22 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 667. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the er311_20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone er311_20 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for er311_20 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. er311_20 demonstrated at least some similarity with sequences identified as AF035526 (*Mus musculus* kanadapin mRNA, complete cds), R18277 (yg01c06.r1 *Homo sapiens* cDNA clone 31018 5' similar to SP:ZK632.2 CE00419 COILED COIL PROTEIN), R47371 (Hf060-r *Homo sapiens* cDNA clone f060-r), and Z40133 (*H. sapiens* partial cDNA sequence; clone c-1sh08). The predicted amino acid sequence disclosed herein for er311_20 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted er311_20 protein demonstrated at least some similarity to sequences identified as AF035526 (kanadapin [*Mus musculus*]) and Z22181 (ZK632.2 [*Caenorhabditis elegans*]). The mouse kanadapin protein and the predicted er311_20 protein both contain poly-glutamic acid stretches within their C-terminal portions. Based upon sequence similarity, er311_20 proteins and each similar protein or peptide may share at least some activity.

The TopPredII computer program predicts two potential transmembrane domains within the er311_20 protein sequence, one centered around amino acid 667 and another at the extreme C-terminus of SEQ ID NO:22.

er311_20 protein was expressed in a COS cell expression system, and an expressed
5 protein band of approximately 91 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "fh149_12"

A polynucleotide of the present invention has been identified as clone "fh149_12".
10 fh149_12 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh149_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
15 as "fh149_12 protein").

The nucleotide sequence of fh149_12 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fh149_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino
20 acids 133 to 145 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fh149_12 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh149_12 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for fh149_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh149_12 demonstrated at least some similarity with sequences
30 identified as AA653557 (ag67b07.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1127989 3'), AA191185 (zq45b09.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632633 5'), H20588 (yn63d06.r1 Homo sapiens cDNA clone 173099 5'), R16294 (yf93b09.r1 Homo sapiens cDNA clone 30087 5'), T08702 (Rat OCT-1 gene),

T25120 (Human gene signature HUMGS07278), U38652 (Mus musculus transmembrane transporter (Lx1) mRNA, complete cds), U77086 (Human organic cation transporter 1 (hOCT1) mRNA, complete cds), and Z66539 (H.sapiens creatine transporter gene). The predicted amino acid sequence disclosed herein for fh149_12 was searched against the
5 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh149_12 protein demonstrated at least some similarity to sequences identified as D17546 (Collagen [Mus musculus]), R77676 (Rat OCT-1 protein), and U77086 (organic cation transporter 1 [Homo sapiens]). The fh149_12 protein also shows
10 some homology to organic cation transporters from rat (GenBank L27651) and pig (GenBank Y09400) cells. Based upon sequence similarity, fh149_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eleven potential transmembrane domains within the fh149_12 protein sequence, centered around amino acids 40, 112, 139, 162, 200, 229, 349, 376, 405, 436, and 467 of SEQ ID NO:24, respectively.

15

Clone "pc201_6"

A polynucleotide of the present invention has been identified as clone "pc201_6". pc201_6 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat.
20 No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pc201_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pc201_6 protein").

The nucleotide sequence of pc201_6 as presently determined is reported in SEQ
25 ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pc201_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 20 to 32 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature
30 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pc201_6 protein.

A partial cDNA clone related to pc201_6, pc201_SP, was also isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The pc201_SP clone appears to encode a splice variant of the pc201_6 protein. The amino acid sequence of the predicted pc201_SP splice variant protein comprises the amino acid sequence reported in SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pc201_6 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for pc201_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pc201_6 demonstrated at least some similarity with sequences identified as AA256414 (zr80d11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 682005 5' similar to WP EEED8.9 CE01893), AA342139 (EST47690 Fetal spleen Homo sapiens cDNA 3' end), AC004085 (Homo sapiens; HTGS phase 1, 72 unordered pieces), AF035950 (Homo sapiens putative DDB p127-associated protein mRNA, partial cds), and H10436 (ym08d09.s1 Homo sapiens cDNA clone 47394 3'). The predicted amino acid sequence disclosed herein for pc201_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pc201_6 protein demonstrated at least some similarity to sequences identified as AF035950 (putative DDB p127-associated protein [Homo sapiens]) and U23484 (EEED8.5 [Caenorhabditis elegans]). Based upon sequence similarity, pc201_6 proteins and each similar protein or peptide may share at least some activity.

Clone "pl87_1"

A polynucleotide of the present invention has been identified as clone "pl87_1". pl87_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl87_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl87_1 protein").

The nucleotide sequence of pl87_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl87_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pl87_1 should be approximately 700 bp.

The nucleotide sequence disclosed herein for pl87_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl87_1 demonstrated at least some similarity with sequences
10 identified as AA371861 (EST83927 Parathyroid gland tumor I Homo sapiens cDNA 5' end) and AA861863 (ak39e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408364 3'). Based upon sequence similarity, pl87_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domains within the pl87_1 protein sequence centered around amino acid
15 50 of SEQ ID NO:28.

pl87_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

20 Clone "pm514_4"

A polynucleotide of the present invention has been identified as clone "pm514_4". pm514_4 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
25 of computer analysis of the amino acid sequence of the encoded protein. pm514_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm514_4 protein").

The nucleotide sequence of pm514_4 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the pm514_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm514_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for pm514_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm514_4 demonstrated at least some similarity with sequences identified as AA393855 (zv64g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758468 5' similar to WP ZK1248.14 CE02898), AA427943 (zw53d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 3'), AA434561 (zw53d10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 5'), W49736 (zc41a03.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324844 5'), and U95822 (Human putative transmembrane GTPase mRNA, partial cds). The predicted amino acid sequence disclosed herein for pm514_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm514_4 protein demonstrated at least some similarity to sequences identified as U95822 (putative transmembrane GTPase [Homo sapiens]). Based upon sequence similarity, pm514_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm514_4 protein sequence, centered around amino acid 600 of SEQ ID NO:30.

Clone "co155_12"

A polynucleotide of the present invention has been identified as clone "co155_12". co155_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. co155_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co155_12 protein").

The nucleotide sequence of co155_12 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the co155_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the co155_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co155_12 should be approximately 2700 bp.

5 The nucleotide sequence disclosed herein for co155_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co155_12 demonstrated at least some similarity with sequences identified as AA578373 (nl23d11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1041525, mRNA sequence), N43800 (yy42h09.r1 Homo sapiens cDNA clone 10 273953 5'), and W40418 (zc82c10.r1 Pancreatic Islet Homo sapiens cDNA clone 328818 5', mRNA sequence). The predicted amino acid sequence disclosed herein for co155_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted co155_12 protein demonstrated at least some similarity to the sequences identified as L12721 (transmembrane domain encoded by 15 1099-1167) and AF004849 (human serine/threonine protein kinase). Based upon sequence similarity, co155_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential trans-membrane domains within the co155_12 protein sequence, centered around amino acids 90, 180, 470, 580, and 610 of SEQ ID NO:32, respectively.

20

Clone "fn189_13"

A polynucleotide of the present invention has been identified as clone "fn189_13". fn189_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 25 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fn189_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fn189_13 protein").

The nucleotide sequence of fn189_13 as presently determined is reported in SEQ 30 ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fn189_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 9 to 21 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted

mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fn189_13 protein.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fn189_13 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for fn189_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fn189_13 demonstrated at least some similarity with sequences
10 identified as AA144270 (mr14d12.r1 Soares mouse 3NbMS Mus musculus cDNA clone 597431 5') and N27605 (yx44e10.r1 Homo sapiens cDNA clone 264618 5'). The predicted amino acid sequence disclosed herein for fn189_13 was searched against the GenPept, GeneSeq, and SWISS_PROT amino acid sequence databases using the BLASTX search protocol. The predicted fn189_13 protein demonstrated at least some similarity to
15 sequences identified as P32857 (PROTEIN PTM1 PRECURSOR [Saccharomyces cerevisiae]) and U64598 (weakly similar to S. cerevisiae PTM1 precursor (SP:P32857) [Caenorhabditis elegans]). Based upon sequence similarity, fn189_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the fn189_13
20 protein sequence, centered around amino acids 225, 260, 340, 360, and 420 of SEQ ID NO:34, respectively.

Clone "lv2_47"

A polynucleotide of the present invention has been identified as clone "lv2_47".
25 lv2_47 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. lv2_47 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
30 "lv2_47 protein").

The nucleotide sequence of lv2_47 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lv2_47 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. The TopPredII

computer program predicts a potential transmembrane domain within the lv2_47 protein sequence of SEQ ID NO:36, centered around amino acid 60.

Another potential lv2_47 reading frame and predicted amino acid sequence is encoded by basepairs 365 to 880 of SEQ ID NO:35 and is reported in SEQ ID NO:178.

5 Amino acids 49 to 61 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:178. The TopPredII computer program predicts two additional potential
10 transmembrane domains within the SEQ ID NO:178 amino acid sequence.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lv2_47 should be approximately 1950 bp.

The nucleotide sequence disclosed herein for lv2_47 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
15 FASTA search protocols. lv2_47 demonstrated at least some similarity with sequences identified as AA007293 (zh97f07.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429253 5'), AA447347 (zw93g06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784570 5' similar to WP:F43E2.7 CE07243), AA522451 (ng30h09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:936353), AA526614 (ni52g12.s1
20 NCI_CGAP_Ov2 Homo sapiens cDNA clone 980518), F18178 (H.sapiens EST sequence (002-T4-28) from skeletal muscle, mRNA sequence), H46569 (yo20f10.s1 Homo sapiens cDNA clone 178507 3'), and T22574 (Human gene signature HUMGS04190). Based upon sequence similarity, lv2_47 proteins and each similar protein or peptide may share at least some activity.

25

Clone "ml243_1"

A polynucleotide of the present invention has been identified as clone "ml243_1". ml243_1 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.
30 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml243_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml243_1 protein").

The nucleotide sequence of ml243_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml243_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 25 to 37 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml243_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml243_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml243_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml243_1 demonstrated at least some similarity with sequences identified as N66656 (yy71a06.s1 Homo sapiens cDNA clone 278962 3'), R17513 (yg02g12.r1 Homo sapiens cDNA clone 31064 5'), Z83837 (Human DNA sequence from Fosmid 113D11 on chromosome 22q11.2-qter contains ESTs, CpG island), and Z84468 (Human DNA sequence from clone 299D3; HTGS phase 1). Based upon sequence similarity, ml243_1 proteins and each similar protein or peptide may share at least some activity.

ml243_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "pm96_9"

A polynucleotide of the present invention has been identified as clone "pm96_9". pm96_9 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm96_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm96_9 protein").

The nucleotide sequence of pm96_9 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm96_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm96_9 should be approximately 3600 bp.

The nucleotide sequence disclosed herein for pm96_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm96_9 demonstrated at least some similarity with sequences
10 identified as AA444024 (zv44d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756503 5'), AA488901 (aa55h09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824897 3'), R16408 (yf40b02.r1 Homo sapiens cDNA clone 129291 5'), T19732 (Human gene signature HUMGS00806), U52112 (Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1
15 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene), and Z82250 (Human DNA sequence from cosmid N86D4 on chromosome 22q12-qter contains STS). Based upon sequence similarity, pm96_9 proteins and each similar protein
20 or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the extreme C-terminus of the pm96_9 protein sequence (SEQ ID NO:40).

Clone "pu261_1"

25 A polynucleotide of the present invention has been identified as clone "pu261_1". pu261_1 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.
30 pu261_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu261_1 protein").

The nucleotide sequence of pu261_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the pu261_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 116 to 128 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 129. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pu261_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu261_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pu261_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu261_1 demonstrated at least some similarity with sequences identified as H16093 (ym20g10.r1 Homo sapiens cDNA clone 48582 5'). Based upon sequence similarity, pu261_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the pu261_1 protein sequence centered around amino acid 70 of SEQ ID NO:42.

Clone "pw214_15"

A polynucleotide of the present invention has been identified as clone "pw214_15". pw214_15 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw214_15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw214_15 protein").

The nucleotide sequence of pw214_15 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw214_15 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw214_15 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw214_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. pw214_15 demonstrated at least some similarity with sequences identified as AA173391 (zp03a07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595284 5'), AA253067 (zr52a10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 667002 5'), AA523652 ni64d09.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone 981617), and H41832 (yo07b08.r1 Homo sapiens cDNA clone 177207 5'). Based upon sequence similarity, pw214_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw214_15 protein sequence centered around amino acid 15 of SEQ ID NO:44.

10

Clone "qb56_19"

A polynucleotide of the present invention has been identified as clone "qb56_19". qb56_19 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qb56_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qb56_19 protein").

The nucleotide sequence of qb56_19 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qb56_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 18 to 40 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qb56_19 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qb56_19 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qb56_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qb56_19 demonstrated at least some similarity with sequences identified as AA632658 (np87c12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone

IMAGE:1133302), N56430 (JJ8973F Homo sapiens cDNA clone JJ8973 5'), and W05470 (za87f11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299565 5'). Based upon sequence similarity, qb56_19 proteins and each similar protein or peptide may share at least some activity.

- 5 qb56_19 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "qc646_1"

- 10 A polynucleotide of the present invention has been identified as clone "qc646_1". qc646_1 was isolated from a human adult neural tissue (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded
- 15 protein. qc646_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc646_1 protein").

- The nucleotide sequence of qc646_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qc646_1 protein
- 20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 12 to 24 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Amino acids 32 to 44 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 45, or are a transmembrane domain. Due to the hydrophobic
- 25 nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the qc646_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc646_1 should be approximately 1800 bp.

- The nucleotide sequence disclosed herein for qc646_1 was searched against the
- 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc646_1 demonstrated at least some similarity with sequences identified as AA470035 (zt94a07.r1 Soares testis NHT Homo sapiens cDNA clone 729972 5'), and AA483957 (ne76e11.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone

IMAGE:910220). The predicted amino acid sequence disclosed herein for qc646_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qc646_1 protein demonstrated at least some similarity to sequences identified as D88666 (PS-PLA1 (serine phospholipid-specific phospholipase A) [Rattus norvegicus]), M93284 (lipase related protein 2 [Homo sapiens]), and R30739 (C-terminally truncated GPL(1-319)), as well as lipases from various other species. Rat PS-PLA1, serine phospholipid-specific phospholipase A, is a member of the lipase family and is secreted from activated platelets. Based upon sequence similarity, qc646_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the qc646_1 protein sequence, one centered around amino acid 190 and another around amino acid 325 of SEQ ID NO:48. The nucleotide sequence of qc646_1 indicates that it may contain Alu repetitive elements.

Clone "qf116_2"

A polynucleotide of the present invention has been identified as clone "qf116_2". qf116_2 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf116_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf116_2 protein").

The nucleotide sequence of qf116_2 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf116_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf116_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qf116_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf116_2 demonstrated at least some similarity with sequences identified as D50810 (placental leucine aminopeptidase [Homo sapiens]), R94512 (GTVap (short version), insulin-cleaving aminopeptidase from GLUT-4 vesicles), and U32990

(vp165 [Rattus norvegicus]). Human placental leucine aminopeptidase/oxytocinase (P-LAP), a member of the type II membrane-spanning zinc metallopeptidase family, degrades several peptide hormones such as oxytocin and vasopresin, suggesting a role in maintaining homeostasis during pregnancy. The predicted P-LAP amino acid sequence contains the HEXXH consensus sequence of zinc metallopeptidases, indicating that the enzyme belongs to this family, which includes aminopeptidase N and aminopeptidase A. The deduced P-LAP amino acid sequence also contains a hydrophobic region near the N-terminus, suggesting that the enzyme is a type II integral membrane protein. Results suggest that the enzyme is synthesized as an integral membrane protein and is released into blood under some physiological conditions. (See Rogi *et al.*, 1996, *J. Biol. Chem.* 271(1): 56-61, which is incorporated by reference herein.) Based upon sequence similarity, qf116_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the qf116_2 protein sequence, one centered around amino acid 25 and another around amino acid 290 of SEQ ID NO:50.

Clone "qf662_3"

A polynucleotide of the present invention has been identified as clone "qf662_3". qf662_3 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf662_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf662_3 protein").

The nucleotide sequence of qf662_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf662_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 133 to 145 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qf662_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf662_3 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for qf662_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf662_3 demonstrated no significant similarity with sequences in these databases. The nucleotide sequence of qf662_3 indicates that it may contain repetitive elements.

Clone "am748_5"

A polynucleotide of the present invention has been identified as clone "am748_5". am748_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. am748_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "am748_5 protein").

The nucleotide sequence of am748_5 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am748_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 14 to 26 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the am748_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am748_5 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for am748_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am748_5 demonstrated at least some similarity with sequences identified as AA418860 (zv98g04.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767862 5' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element; contains element PTR5 repetitive element), AC003007 (Human

Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence), H73304 (yu27c10.r1 Homo sapiens cDNA clone 235026 5' similar to contains Alu repetitive element), N35175 (yx83d10.r1 Homo sapiens cDNA clone 268339 5' similar to gb X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element),
5 N41479 (yy05a11.r1 Homo sapiens cDNA clone 270332 5' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN)), Q81139 (HPLA2-8 gene), T04964 (EST02852 Homo sapiens cDNA clone HFBCI77), and U18391 (Human Alu sequence clone A8). The predicted amino acid sequence disclosed herein for am748_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.
10 The predicted am748_5 protein demonstrated at least some similarity to sequences identified as X55777 (put. ORF [Homo sapiens]) and R13556 (Protein encoded downstream of hhc_M oncoprotein). Based upon sequence similarity, am748_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of am748_5 indicates that it may contain one or more of the following repetitive
15 elements: Alu, L1.

Clone "cj507_1"

A polynucleotide of the present invention has been identified as clone "cj507_1". cj507_1 was isolated from a human fetal brain cDNA library using methods which are
20 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj507_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj507_1 protein").

25 The nucleotide sequence of cj507_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj507_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 cj507_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for cj507_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj507_1 demonstrated at least some similarity with sequences

identified as AA100356 (zn46a02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550442 5' similar to contains element PTR5 repetitive element), AA228100 (zr56g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667446 3'), AA479997 (zv18b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753973 5' similar to contains
5 element PTR5 repetitive element, mRNA sequence), and X85324 (H.sapiens mRNA for non polymorphic CAG repeat (CAG12)). Based upon sequence similarity, cj507_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cj507_1 protein sequence centered around amino acid 265 of SEQ ID NO:56. The
10 nucleotide sequence of cj507_1 indicates that it may contain a GCA simple repeat region.

cj507_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 47 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "cn922_5"

A polynucleotide of the present invention has been identified as clone "cn922_5". cn922_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
20 analysis of the amino acid sequence of the encoded protein. cn922_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cn922_5 protein").

The nucleotide sequence of cn922_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the cn922_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cn922_5 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for cn922_5 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cn922_5 demonstrated at least some similarity with sequences identified as H34191 (EST110864 Rattus sp. cDNA 5' end), R18707 (yf98f02.r1 Homo sapiens cDNA clone 30546 5'), T26556 (Human gene signature HUMGS08801), and

Z83230 (*Caenorhabditis elegans* cosmid F56A8). The predicted amino acid sequence disclosed herein for cn922_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cn922_5 protein demonstrated at least some similarity to sequences identified as AB004535
5 (HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION [Schizosaccharomyces pombe]) and Z83230 (F56A8.a and F56A8.1 [*Caenorhabditis elegans*]). Based upon sequence similarity, cn922_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the cn922_5 protein sequence, centered around
10 amino acids 25, 100, 135, 190, 290, and 370 of SEQ ID NO:58, respectively. The nucleotide sequence of cn922_5 indicates that it may contain one or more of the following repetitive elements: MER, L1.

Clone "cw691_11"

15 A polynucleotide of the present invention has been identified as clone "cw691_11". cw691_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw691_11 is a full-length
20 clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw691_11 protein").

The nucleotide sequence of cw691_11 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw691_11 protein
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

Another potential cw691_11 reading frame and predicted amino acid sequence is encoded by basepairs 542 to 970 of SEQ ID NO:59 and is reported in SEQ ID NO:179. Amino acids 34 to 46 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the
30 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw691_11 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for cw691_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw691_11 demonstrated at least some similarity with sequences identified as AA363712 (EST74158 Pancreas I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein R10E12.1), AA521201 (aa74c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 826674 3'), AA527142 (ni07a10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE 967290, mRNA sequence), AA745501 (ny64d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283045, mRNA sequence), N73108 (yv69a09.r1 Homo sapiens cDNA clone 247960 5'), T19938 (Human gene signature HUMGS01070), and W77963 (zd70d09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346001 5' similar to WP:R10E12.1 CE00310). The predicted amino acid sequence disclosed herein for cw691_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw691_11 protein demonstrated at least some similarity to sequences identified as P82971 (Bioadhesive precursor protein from cDNA 52), U73679 (YNK1-a [Caenorhabditis elegans]), and Z29561 (R10E12.1 [Caenorhabditis elegans]). Based upon sequence similarity, cw691_11 proteins and each similar protein or peptide may share at least some activity.

Clone "cw1000_2"

A polynucleotide of the present invention has been identified as clone "cw1000_2". cw1000_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1000_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1000_2 protein").

The nucleotide sequence of cw1000_2 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1000_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino

acids 24 to 36 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the
5 cw1000_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1000_2 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cw1000_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
10 FASTA search protocols. cw1000_2 demonstrated at least some similarity with sequences identified as AA446779 (zw89d11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784149 5', mRNA sequence), AA493561 (nh04f07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone 943333 similar to WP:F15G9.4 CE01552 IG SUPERFAMILY REPEATS ;contains element MSR1 repetitive element), H35690 (EST111696 Rattus sp.
15 cDNA similar to Opioid binding protein/cell adhesion-like molecule), R18502 (yf96a05.r1 Homo sapiens cDNA clone 30376 5'), T21582 (Human gene signature HUMGS02965), T39504 (ya06g11.r1 Homo sapiens cDNA clone 60740 5'), T46848 (yb94b01.r1 Homo sapiens cDNA clone 78793 5'), T51129 (yb94b01.s1 Homo sapiens cDNA clone 78793 3'), and W67535 (zd40g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
20 343172 3' similar to PIR S05539 S05539 glycophorin C - human ;contains element MSR1 repetitive element). The predicted amino acid sequence disclosed herein for cw1000_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1000_2 protein demonstrated at least some similarity to sequences identified as M24406 (poliovirus receptor [Homo sapiens]),
25 R07130 (H20B receptor), W04404 (Human CRTAM; Cytotoxic or Regulatory T-cell associated Mol.; CRTAM), X13890 (glycophorin C [Homo sapiens]), and X90569 (elastic titin [Homo sapiens]). Based upon sequence similarity, cw1000_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the cw1000_2
30 protein sequence centered around amino acid 358 of SEQ ID NO:62. The nucleotide sequence of cw1000_2 indicates that it may contain a GCC1 repeat element.

cw1000_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 57 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "cw1640_1"

A polynucleotide of the present invention has been identified as clone "cw1640_1". cw1640_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. cw1640_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1640_1 protein").

The nucleotide sequence of cw1640_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the cw1640_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 123 to 135 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 136. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1640_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1640_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cw1640_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1640_1 demonstrated at least some similarity with sequences identified as AA075643 (zm88a12.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544990 5' similar to SW:ACT_EUPCR P20360 ACTIN), AA411334 (zv29e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755084 5' similar to
30 WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN), AA913364 (ol37b07.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525621 3' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN, mRNA sequence), N25416 (yx40g10.r1 Homo sapiens cDNA clone 264258 5' similar to SP ACT2_PLAFA P14883 ACTIN), R96887

(yq61g10.r1 Homo sapiens cDNA clone 200322 5'), W37097 (zb98h03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 5'), W44778 (zb98h03.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 3'), W61038 (zc54g09.r1 Soares senescent fibroblasts NbHSF Homo), W76570 (zd66f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345647 5' similar to SW:ACT_PROCL P45521 ACTIN), and W82519 (mf05b01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for cw1640_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1640_1 protein demonstrated at least some similarity to sequences identified as J00068 (alpha-actin [Homo sapiens]), J01163 (actin [Oxytricha fallax]), R22026 (A. chrysogenum actin), R50328 (Drug resistant structural protein), U42436 (Similar to actin-like protein [Caenorhabditis elegans]), and U90439 (actin isolog [Arabidopsis thaliana]). Based upon sequence similarity, cw1640_1 proteins and each similar protein or peptide may share at least some activity.

Clone "d24_1"

A polynucleotide of the present invention has been identified as clone "d24_1". A cDNA clone was first isolated from a human adult blood (peripheral blood mononuclear cells treated with concanavalin A and phorbol myristate acetate) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate d24_1 from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin, phorbol myristate acetate, and mixed lymphocyte reaction) cDNA library. d24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "d24_1 protein").

The nucleotide sequence of d24_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the d24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 124 to 136 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 137. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the d24_1 protein. The mRNA sequence encoding amino acids 172 to 175 of SEQ ID NO:66 may not be present in alternatively-spliced forms of d24_1 mRNA molecules.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
5 d24_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for d24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. d24_1 demonstrated at least some similarity with sequences identified as AA478740 (zv14g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
10 753670 3'), AA479444 (zv14g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 5', mRNA sequence), AA278581 (zs76f09.r1 Soares NbHTGBC Homo sapiens cDNA clone 703433 5' similar to WP T04A8.12 CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), H05202 (yl85h02.r1 Homo sapiens cDNA clone 45213 5' similar to SP T04A8.12m CE01067 YEAST 107.9KD
15 PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), R74287 (yi57e07.r1 Homo sapiens cDNA clone 143364 5'), U57715 (*Rattus norvegicus* FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete CDs), and Z35663 (*C. elegans* protein of unknown function). The predicted amino acid sequence disclosed herein for d24_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
20 BLASTX search protocol. The predicted d24_1 protein demonstrated at least some similarity to the sequence identified as U57715 (FGF receptor activating protein FRAG1 [*Rattus norvegicus*]). Lorenzi *et al.* (1996, *Proc. Natl. Acad. Sci. USA* 93:8956, incorporated by reference herein) studied the FRAG1 gene in rat osteosarcoma cells. They concluded that the FRAG1 gene product gets fused to FGF receptor 2 (FGFR2). This
25 fusion "drastically stimulates the transforming activity and autophosphorylation of the receptor" and causes oncogenicity. Based upon sequence similarity, d24_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the d24_1 protein sequence, centered around amino acids 34, 154, and 194 of SEQ ID NO:66,
30 respectively.

d24_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "dd426_1"

A polynucleotide of the present invention has been identified as clone "dd426_1". A cDNA clone was first isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dd426_1 from a human adult testes (teratocarcinoma NCCIT) cDNA library. dd426_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd426_1 protein").

The nucleotide sequence of dd426_1 as presently determined is reported in SEQ
15 ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd426_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 76 to 88 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 89. Due to the hydrophobic nature
20 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd426_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd426_1 should be approximately 800 bp.

25 The nucleotide sequence disclosed herein for dd426_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd426_1 demonstrated at least some similarity with sequences identified as AA760716 (nz13d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287659 similar to WP:F13H10.3 CE05624 YEAST YEH4 LIKE PROTEIN;
30 mRNA sequence), H11919 (ym10e10.r1 Homo sapiens cDNA clone 47462 5'), and Z68748 (Caenorhabditis elegans cosmid F13H10). The predicted amino acid sequence disclosed herein for dd426_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd426_1 protein

demonstrated at least some similarity to sequences identified as U39782 (lysine and histidine specific transporter [*Arabidopsis thaliana*]) and Z68748 (F13H10.3 [*Caenorhabditis elegans*]). Based upon sequence similarity, dd426_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program
5 predicts an additional potential transmembrane domain within the dd426_1 protein sequence centered around amino acid 30 of SEQ ID NO:68, which may also function as a leader/signal sequence.

dd426_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 12 kDa was detected in membrane fractions using SDS
10 polyacrylamide gel electrophoresis.

Clone "di393_2"

A polynucleotide of the present invention has been identified as clone "di393_2". di393_2 was isolated from a human adult testes cDNA library using methods which are
15 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. di393_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "di393_2 protein").

20 The nucleotide sequence of di393_2 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the di393_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 7 to 19 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted
25 mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the di393_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 di393_2 should be approximately 600 bp.

The nucleotide sequence disclosed herein for di393_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. di393_2 demonstrated at least some similarity with sequences

identified as AA669506 (zu85g08.s1 Soares testis NHT Homo sapiens cDNA clone 744830 3', mRNA sequence). Based upon sequence similarity, di393_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the di393_2 protein sequence centered around amino acid 66 of SEQ ID NO:70.

di393_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 20 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "dj167_2"

A polynucleotide of the present invention has been identified as clone "dj167_2". dj167_2 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167_2 protein").

The nucleotide sequence of dj167_2 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167_2 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for dj167_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dj167_2 demonstrated at least some similarity with sequences identified as H49161 (yq18d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274208 5'), L12350 (Human thrombospondin 2 (THBS2) mRNA, complete cds), T98917 (ye66b03.s1 Homo sapiens cDNA clone 122669 3' similar to SP:TSP1_CHICK P35440 THROMBOSPONDIN 1), and X87620 (B.taurus mRNA for complete thrombospondin). The predicted amino acid sequence disclosed herein for dj167_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dj167_2 protein demonstrated at least some

similarity to sequences identified as L12350 (thrombospondin 2 [Homo sapiens]), M60853 (thrombospondin [Gallus gallus]), R40823 (Human thrombospondin 1), U48245 (protein kinase C-binding protein Nel [Rattus norvegicus]), X87620 (thrombospondin [Bos taurus]), and Z71178 (B0024.14 [Caenorhabditis elegans]). Based upon sequence
5 similarity, dj167_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dj167_2 protein sequence, centered around amino acids 140, 215, and 315 of SEQ ID NO:72, respectively.

10 Clone "dj167_19"

A polynucleotide of the present invention has been identified as clone "dj167_19". dj167_19 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
15 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167_19 protein").

The nucleotide sequence of dj167_19 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the dj167_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 22 to 34 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
25 should the predicted leader/signal sequence not be separated from the remainder of the dj167_19 protein. The dj167_19 clone is related to that of dj167_2, and extends further 5'. The dj167_19 clone appears to contain coding sequences for chorionic somatomammotropin in the opposite orientation at its 5' end between Sfi restriction sites (at nucleotides 16 and 839 of SEQ ID NO:73). The dj167_2 and dj167_19 clones may represent
30 alternatively spliced messenger RNA molecules encoding two different forms of a secreted protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167_19 should be approximately 4500 bp.

Analysis of the dj167_19 amino acid sequence (SEQ ID NO:74) reveals the following domains: IGFBP cysteine-rich domain at amino acids 60-75; VWF-B cysteine-rich domains at amino acids 174-210, 212-247, 255-291, and 293-328; Chordin cysteine-rich domains at amino acids 336-390, 403-456, 608-662, 679-734, 753-808, and 819-873; Antistatin (protease inhibitor) cysteine-rich domains at amino acids 469-498, 505-532, 539-564, and 567-592; RGD cell attachment sequence at amino acids 314-316, and Asn glycosylation sites at amino acids 71, 113, 330, 474, and 746. The cysteine-rich domains listed above are similar to domains found in the C domain of Von Willebrand Factor (VWF), and in procollagen and thrombospondin. In addition, the amino acid sequence of SEQ ID NO:74 from amino acid 938 to amino acid 960 appears to be a transmembrane domain.

The dj167_19 transcript is expressed in several cell types, including kidney, pancreas, spleen, and ovary, and is most abundantly expressed in placental tissue.

Clone "dw665_4"

A polynucleotide of the present invention has been identified as clone "dw665_4". dw665_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dw665_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw665_4 protein").

The nucleotide sequence of dw665_4 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dw665_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 15 to 27 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Amino acids 16 to 28 of SEQ ID NO:76 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence in that case beginning at amino acid 29. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dw665_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw665_4 should be approximately 3750 bp.

The nucleotide sequence disclosed herein for dw665_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw665_4 demonstrated at least some similarity with sequences identified as AA029053 (zk09f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470051 3'), H77289 (EST27017 WATM1 Homo sapiens cDNA clone 27017, mRNA sequence), and T21722 (Human gene signature HUMGS03170). The predicted amino acid sequence disclosed herein for dw665_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dw665_4 protein demonstrated at least some similarity to sequences identified as L35764 (chordin [Xenopus laevis]) and W31559 (Xenopus frog protein "chordin"). Analysis of motifs within the predicted dw665_4 protein revealed the presence of Chordin cysteine-rich domains at amino acids 37-99, 115-178, and 260-322 of SEQ ID NO:76; an 'RGD' cell-attachment sequence (at amino acids 179-181 of SEQ ID NO:76), which in some proteins has been shown to play a role in cell adhesion; and Asp glycosylation sites at amino acids 118 and 291. Based upon sequence similarity, dw665_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dw665_4 indicates that it may contain an AC repetitive element.

dw665_4 transcripts are expressed in many tissues including kidney, adrenal gland, and prostate tissues, and are most abundantly expressed in pancreas; however, little or no dw665_4 transcript expression is observed in liver or peripheral blood cells. dw665_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis; two additional bands at approximately 26 and 30 kDa were also observed. BIACORE binding experiments indicate that dw665_4 protein has a Chordin-like protein-binding profile, and binds to BMP-2, BMP-4, BMP-7, BMP-12, and GDF-5.

Clone "dx146_12"

A polynucleotide of the present invention has been identified as clone "dx146_12". dx146_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx146_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx146_12 protein").

The nucleotide sequence of dx146_12 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the dx146_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx146_12 should be approximately 2250 bp.

The nucleotide sequence disclosed herein for dx146_12 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx146_12 demonstrated at least some similarity with sequences identified as AA090429 (y0527.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), AA232068 (zr24a01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664296 5'), AA886679 (oj47h07.s1 NCI_CGAP_Kid3 Homo sapiens
15 cDNA clone IMAGE:1501501 3' similar to WP:F16A11.2 CE09424 METHANOCOCCUS HYPOTHETICAL PROTEIN 0682 LIKE; mRNA sequence), R61436 (yh15g06.r1 Homo sapiens cDNA clone 37884 5'), and Z81505 (Caenorhabditis elegans cosmid F16A11, complete sequence). The predicted amino acid sequence disclosed herein for dx146_12 was searched against the GenPept and GeneSeq amino acid sequence
20 databases using the BLASTX search protocol. The predicted dx146_12 protein demonstrated at least some similarity to sequences identified as U67515 (hypothetical protein (SP P46850) [Methanococcus jannaschii]) and Z81505 (F16A11.2 [Caenorhabditis elegans]). Based upon sequence similarity, dx146_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a
25 potential transmembrane domain within the dx146_12 protein sequence centered around amino acid 405 of SEQ ID NO:78.

dx146_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 50 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

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Clone "dx219_13"

A polynucleotide of the present invention has been identified as clone "dx219_13". dx219_13 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
5 analysis of the amino acid sequence of the encoded protein. dx219_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx219_13 protein").

The nucleotide sequence of dx219_13 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the dx219_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 94 to 106 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 107. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
15 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dx219_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx219_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for dx219_13 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx219_13 demonstrated at least some similarity with sequences identified as AA429731 (zw66g05.s1 Soares testis NHT Homo sapiens cDNA clone 781208 3'), AA446067 (zw66e06.r1 Soares testis NHT Homo sapiens cDNA clone 781186 5', mRNA sequence), T23212 (standard; cDNA to mRNA; 161 BP, Human gene signature
25 HUMGS05005), W29299 (mb99f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 337565 5'), W87852 (zh68b05.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417201 5'), and Y13897 (Homo sapiens partial mRNA for hypothetical protein). Based upon sequence similarity, dx219_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two
30 additional potential transmembrane domains within the dx219_13 protein sequence, one centered around amino acid 160 and another around amino acid 275 of SEQ ID NO:80.

dx219_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 37 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "fm3_1"

A polynucleotide of the present invention has been identified as clone "fm3_1". fm3_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. fm3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fm3_1 protein").

The nucleotide sequence of fm3_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the fm3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 7 to 19 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
20 the predicted leader/signal sequence not be separated from the remainder of the fm3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fm3_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for fm3_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fm3_1 demonstrated at least some similarity with sequences identified as T15669 (IB1718 Infant brain, Bento Soares Homo sapiens cDNA 3'end). Based upon sequence similarity, fm3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional
30 potential transmembrane domains within the fm3_1 protein sequence centered around amino acid 85 of SEQ ID NO:82.

fm3_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 9 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "h225_1"

A polynucleotide of the present invention has been identified as clone "h225_1". h225_1 was isolated from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin and phorbol myristate acetate and mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. h225_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "h225_1 protein").

The nucleotide sequence of h225_1 as presently determined is reported in SEQ ID NO:83. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the h225_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 52 to 64 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the h225_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone h225_1 should be approximately 832 bp.

The nucleotide sequence disclosed herein for h225_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. h225_1 demonstrated at least some similarity with sequences identified as AA604374 (no87e01.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1113816 similar to WP:ZK757.1 CE00467; mRNA sequence), H18393 (yn49a12.r1 Homo sapiens cDNA clone 171742 5' similar to SP:ZK757.1 CE00467), and R23642 (yh35e03.r1 Homo sapiens cDNA clone 131740 5'). The predicted amino acid sequence disclosed herein for h225_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted h225_1 protein demonstrated at least some similarity to sequences identified as AL022600 (hypothetical protein [Schizosaccharomyces pombe]) and Z48758 (SC9727_21 unknown [Saccharomyces cerevisiae]). Based upon sequence similarity, h225_1 proteins and each similar protein or peptide may share at least some activity.

Clone "kj320_1"

A polynucleotide of the present invention has been identified as clone "kj320_1". kj320_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kj320_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kj320_1 protein").

The nucleotide sequence of kj320_1 as presently determined is reported in SEQ ID
10 NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kj320_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 26 to 38 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature
15 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the kj320_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kj320_1 should be approximately 4900 bp.

20 The nucleotide sequence disclosed herein for kj320_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kj320_1 demonstrated at least some similarity with sequences identified as A45343 (Sequence 13 from Patent WO9517522), AA284111 (zc36f08.T7 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324423 3' similar to WP
25 ZK688.8 CE00544 UDP-GALNAC; mRNA sequence), AA375707 (EST88026 HSC172 cells II Homo sapiens cDNA 5' end), AA534406 (nf76b08.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 925815), D39885 (Rice cDNA, partial sequence (S1531_1A)), G10010 (human STS CHLC.GCT16E06.P18287 clone GCT16E06), Q75104 (Cattle GalNAc-transferase), Q95187 (Simple tandem repeat (STR) corresponding
30 to wg1d10), and U35890 (Rattus norvegicus polypeptide GalNAc transferase T1 mRNA, complete cds). The predicted amino acid sequence disclosed herein for kj320_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kj320_1 protein demonstrated at least some

similarity to sequences identified as R66397 (Cattle GalNAc-transferase), U41514 (UDP-GalNAc polypeptide N-acetylgalactosaminyltransferase [Homo sapiens]), and X85018 (UDP-GalNAc polypeptide N-acetylgalactosaminyl transferase [Homo sapiens]). Analysis of motifs within kj320_1 reveals the presence of the alpha-2-macroglobulin family thiolester region signature. The proteinase-binding alpha-macroglobulins (A2M) are large glycoproteins found in the plasma of vertebrates, in the hemolymph of some invertebrates, and in reptilian and avian egg white. They inhibit all four classes of proteinases by trapping a proteinase with a peptide stretch containing the specific cleavage site (the 'bait' region) which upon proteinase binding induces a conformational change in the protein, trapping the proteinase. Upon cleavage of the 'bait' region, a covalent bond (a thiol-ester bond between the side chains of a cysteine and a glutamine) is formed between the A2M and the proteinase. Based upon sequence similarity, kj320_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of kj320_1 indicates that it may contain one or more repetitive elements.

kj320_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 136 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "ml236_5"

A polynucleotide of the present invention has been identified as clone "ml236_5". ml236_5 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml236_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml236_5 protein").

The nucleotide sequence of ml236_5 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml236_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 148 to 160 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 161. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a

transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml236_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml236_5 should be approximately 1300 bp.

5 The nucleotide sequence disclosed herein for ml236_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml236_5 demonstrated at least some similarity with sequences identified as AA137204 (zl23h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502821 3'), AA307966 (EST17887 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end, mRNA sequence), AA434504 (zw31c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770884 5' similar to WP C45G9.7 CE01858), AA525971 (ni93g09.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone 984448), AA526490 (ni96c11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE 984692, mRNA sequence), AF028823 (Homo sapiens Tax interaction protein 1 mRNA, partial cds), U90913 (Human clone 23665 mRNA sequence), and W73114 (zd55c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344566 5'). The predicted amino acid sequence disclosed herein for ml236_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml236_5 protein demonstrated at least some similarity to sequences identified as AF028823 (Tax interaction protein 1 [Homo sapiens]) and U21323 (similar to tight junction protein (ZO-1) (SP Z01_HUMAN, Q07157) [Caenorhabditis elegans]). Based upon sequence similarity, ml236_5 proteins and each similar protein or peptide may share at least some activity.

25 ml236_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pu282_10"

30 A polynucleotide of the present invention has been identified as clone "pu282_10". pu282_10 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on

the basis of computer analysis of the amino acid sequence of the encoded protein. pu282_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu282_10 protein").

5 The nucleotide sequence of pu282_10 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu282_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 119 to 131 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 132. Due to the
10 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pu282_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu282_10 should be approximately 1050 bp.

15 The nucleotide sequence disclosed herein for pu282_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu282_10 demonstrated at least some similarity with sequences identified as AA311503 (EST182442 Jurkat T-cells VI Homo sapiens cDNA 5' end), AA336709 (EST41341 Endometrial tumor Homo sapiens cDNA 5' end), AA336890
20 (EST41572 Endometrial tumor), AA385588 (EST99290 Thyroid Homo sapiens cDNA 5' end), AA526889 (ni09e05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:967520), AC003058 (Arabidopsis thaliana "unknown" protein), and T19726 (Human gene signature HUMGS00800). Based upon sequence similarity, pu282_10 proteins and each similar protein or peptide may share at least some activity. The
25 TopPredII computer program predicts two additional potential transmembrane domains within the pu282_10 protein sequence, one centered around amino acid 39 and another around amino acid 95 of SEQ ID NO:90.

pu282_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium
30 and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "at94_2"

A polynucleotide of the present invention has been identified as clone "at94_2". at94_2 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. at94_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "at94_2 protein").

The nucleotide sequence of at94_2 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the at94_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 214 to 226 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 227. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
15 the predicted leader/signal sequence not be separated from the remainder of the at94_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone at94_2 should be approximately 4300 bp.

The nucleotide sequence disclosed herein for at94_2 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. at94_2 demonstrated at least some similarity with sequences identified as N24317 (yx23d12.r1 Homo sapiens cDNA clone 262583 5'), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), and U37026 (Rattus norvegicus brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds). The predicted amino
25 acid sequence disclosed herein for at94_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted at94_2 protein demonstrated at least some similarity to the sequence identified as Z49912 (T24F1.2 [Caenorhabditis elegans]). Based upon sequence similarity, at94_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
30 program predicts four additional potential transmembrane domains within the at94_2 protein sequence, centered around amino acids 23, 306, 332, and 364 of SEQ ID NO:92, respectively.

Clone "bf169_13"

A polynucleotide of the present invention has been identified as clone "bf169_13". bf169_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bf169_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bf169_13 protein").

The nucleotide sequence of bf169_13 as presently determined is reported in SEQ
10 ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bf169_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 342 to 354 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 355. Due to the hydrophobic nature of this
15 possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the bf169_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bf169_13 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for bf169_13 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf169_13 demonstrated at least some similarity with sequences identified as AA227952 (zr56b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667379 3'), AA453914 (zx32e11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788204 5' similar to contains element TAR1 repetitive element; mRNA sequence),
25 H46157 (yo13f11.r1 Homo sapiens cDNA clone 177837 5'), H18792 (yn52e02.r1 Homo sapiens cDNA clone 172058 5'), and N24601 (yx72e01.s1 Homo sapiens cDNA clone 267288 3'). The predicted amino acid sequence disclosed herein for bf169_13 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bf169_13 protein demonstrated at least some
30 similarity to sequences identified as L41834 (plant nuclear protein [Ensis minor]) and Z75539 (F28C1.1 [Caenorhabditis elegans]). Analysis of motifs in the predicted bf169_13 protein revealed a "mitochondrial energy transfer proteins" signature at amino acid 574 of SEQ ID NO:94. Based upon sequence similarity, bf169_13 proteins and each similar

protein or peptide may share at least some activity. The nucleotide sequence of bf169_13 indicates that it may contain one or more GCCCCA, GCCC, GGA and/or GC repeat sequences.

bf169_13 protein was expressed in a COS cell expression system, and an
5 expressed protein band of approximately 109 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "bl152_12"

A polynucleotide of the present invention has been identified as clone "bl152_12".
10 bl152_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bl152_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
15 as "bl152_12 protein").

The nucleotide sequence of bl152_12 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bl152_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bl152_12 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for bl152_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bl152_12 demonstrated at least some similarity with sequences
25 identified as AA280876 (zs97d04.s1 NCI_CGAP_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 3' similar to contains element MER22 repetitive element), AA280956 (zs97d04.r1 NCI_CGAP_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 5'), R21512 (yh19b03.s1 Homo sapiens cDNA clone 130157 3'), R67018 (yi26e05.s1 Homo sapiens cDNA clone 140384 3' similar to contains MER22 repetitive element),
30 R71877 (yj87d11.s1 Homo sapiens cDNA clone 155733 3' similar to contains MER22 repetitive element), T22941 (Human gene signature HUMGS04666), W46539 (zc30g03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323860 3', mRNA sequence), and W70065 (zd49c04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA

clone). The predicted amino acid sequence disclosed herein for bl152_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bl152_12 protein demonstrated at least some similarity to the sequence identified as Z82256 (B0513.2 [Caenorhabditis elegans]). Based upon
5 sequence similarity, bl152_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bl152_12 indicates that it may contain one or more GCC repeat sequences.

bl152_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 25 kDa was detected in conditioned medium using SDS
10 polyacrylamide gel electrophoresis.

Clone "bz578_1"

15 A polynucleotide of the present invention has been identified as clone "bz578_1". bz578_1 was isolated from a human fetal kidney cDNA library using methods and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bz578_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bz578_1 protein").

20 The nucleotide sequence of bz578_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bz578_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 bz578_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for bz578_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bz578_1 demonstrated at least some similarity with sequences identified as T47038 (yb12e08.r1 Homo sapiens cDNA clone 70982 5' contains L1
30 repetitive element) and Z82975 (Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X). The predicted amino acid sequence disclosed herein for bz578_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bz578_1 protein

demonstrated at least some similarity to sequences identified as AF051782 (diaphanous 1 [Homo sapiens]), U96963 (diaphanous 1 [mouse]), and U93572 (putative p150 [Homo sapiens]). Based upon sequence similarity, bz578_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bz578_1 indicates
5 that it may contain one or more L1 repeat sequences.

Clone "cb123_1"

A polynucleotide of the present invention has been identified as clone "cb123_1". cb123_1 was isolated from a human fetal brain cDNA library using methods which are
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cb123_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cb123_1 protein").

15 The nucleotide sequence of cb123_1 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cb123_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 44 to 56 of SEQ ID NO:100 are a predicted leader/signal sequence, with the
20 predicted mature amino acid sequence beginning at amino acid 57. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cb123_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 cb123_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cb123_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cb123_1 demonstrated at least some similarity with sequences identified as AA309020 (EST179803 Colon carcinoma (Caco-2) cell line I Homo sapiens
30 cDNA 5' end, mRNA sequence), R89617 (ym98b08.s1 Homo sapiens cDNA clone 166935 3'), T16814 (NIB1893 Normalized infant brain, Bento Soares Homo sapiens cDNA 3' end similar to EST02882 H. sapiens cDNA clone HFBCL71), T24092 (Human gene signature HUMGS06080), and T55187 (yb43e06.s1 Homo sapiens cDNA clone 73954 3'). The

predicted amino acid sequence disclosed herein for cb123_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cb123_1 protein demonstrated at least some similarity to the sequence identified as U33331 (orf UL133 [Human cytomegalovirus]). Based upon sequence
5 similarity, cb123_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the cb123_1 protein sequence, one centered around amino acid 15 and another around amino acid 80 of SEQ ID NO:100.

10 Clone "ch245_1"

A polynucleotide of the present invention has been identified as clone "ch245_1". ch245_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
15 analysis of the amino acid sequence of the encoded protein. ch245_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ch245_1 protein").

The nucleotide sequence of ch245_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the ch245_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. The TopPredII computer program predicts a potential transmembrane domain within the ch245_1 protein sequence centered around amino acid 87 of SEQ ID NO:102.

Another potential ch245_1 reading frame and predicted amino acid sequence is
25 encoded by basepairs 533 to 778 of SEQ ID NO:101 and is reported in SEQ ID NO:180. The TopPredII computer program predicts a potential transmembrane domain within the SEQ ID NO:180 amino acid sequence centered around amino acid 34 of SEQ ID NO:180.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ch245_1 should be approximately 1350 bp.

30 The nucleotide sequence disclosed herein for ch245_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ch245_1 demonstrated at least some similarity with sequences identified as AA402307 (zu48f03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA

clone 741245 5', mRNA sequence), H19032 (ym44e04.r1 Homo sapiens cDNA clone 50921 5'), H19323 (ym44e04.s1 Homo sapiens cDNA clone 50921 3'), and N36070 (yy02g11.r1 Homo sapiens cDNA clone 270116 5'). The predicted amino acid sequence disclosed herein for ch245_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ch245_1 protein demonstrated at least some similarity to the sequence identified as M58597 (ELAM-1 ligand fucosyltransferase [Homo sapiens]) and U36763 (fatty acid synthase [Mycobacterium bovis]). Based upon sequence similarity, ch245_1 proteins and each similar protein or peptide may share at least some activity.

Clone "cj378_3"

A polynucleotide of the present invention has been identified as clone "cj378_3". cj378_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj378_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj378_3 protein").

The nucleotide sequence of cj378_3 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj378_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj378_3 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cj378_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj378_3 demonstrated at least some similarity with sequences identified as D60138 (Human fetal brain cDNA 5'-end GEN-088A04, mRNA sequence), H19318 (ym44d06.s1 Homo sapiens cDNA clone 51231 3'), H41859 (yo07g06.r1 Homo sapiens cDNA clone 177274 5'), T25386 (Human gene signature HUMGS07551), and T75383 (yc89g05.r1 Homo sapiens cDNA clone 23351 5'). Based upon sequence

similarity, cj378_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the N-terminus of the the cj378_3 protein sequence (SEQ ID NO:104).

5 Clone "cw1481_1"

A polynucleotide of the present invention has been identified as clone "cw1481_1". cw1481_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. cw1481_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1481_1 protein").

The nucleotide sequence of cw1481_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the cw1481_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1481_1 should be approximately 2380 bp.

The nucleotide sequence disclosed herein for cw1481_1 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1481_1 demonstrated at least some similarity with sequences identified as AA027927 (zk05a10.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 5'), AA027928 (zk05a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 3' similar to contains MER28.b2 MER28 repetitive element),
25 AA113357 (zn69g06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563482 3'), AA252304 (zs12b08.s1 Soares NbHTGBC Homo sapiens cDNA clone 684951 3' similar to contains element MER22 repetitive element), AA976744 (oq09a09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE 1585816 3' similar to TR O15025 O15025 KIAA0308 ;contains element MER22 repetitive element; mRNA sequence),
30 R55084 (yg87a06.r1 Homo sapiens cDNA clone 40244 5'), U00930 (Human clone C4E 1.63 (CAC)_n/(GTG)_n repeat-containing mRNA), U00955 (Human clone CE29 8.1 (CAC)_n/(GTG)_n repeat-containing mRNA), and W16808 (zb93a09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320344 3'). The predicted amino acid sequence

disclosed herein for cw1481_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1481_1 protein demonstrated at least some similarity to sequences identified as AB002306 (KIAA0308 [Homo sapiens]), X15906 (precursor polypeptide), and Z68751 (F01G4.1 [Caenorhabditis elegans]). Based upon sequence similarity, cw1481_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cw1481_1 protein sequence centered around amino acid 431 of SEQ ID NO:106, and a putative transmembrane domain within the cw1481_1 protein sequence centered around amino acid 395 of SEQ ID NO:106. The amino acid sequence of cw1481_1 indicates that it has a histidine-rich region and a serine-rich region, and it is strongly internally repeated.

Clone "dd119_4"

A polynucleotide of the present invention has been identified as clone "dd119_4". dd119_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd119_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd119_4 protein").

The nucleotide sequence of dd119_4 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd119_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 27 to 39 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd119_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd119_4 should be approximately 3350 bp.

The nucleotide sequence disclosed herein for dd119_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. dd119_4 demonstrated at least some similarity with sequences identified as AA151924 (zo30e05.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588416 5' similar to SW SLIT_DROME P24014 SLIT PROTEIN PRECURSOR; mRNA sequence), AA193464 (zr41c06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665962 3'), AB011135 (Homo sapiens mRNA for KIAA0563 protein, complete cds), G23888 (human STS WI-12393), H04996 (yl74c12.s1 Homo sapiens cDNA clone 43851 3'), M86526 (Rat proline-rich protein (PRP) gene, 5' end, and containing several Alu-like repetitive elements), M86514 (Rat proline-rich protein mRNA, 3' end), W68823 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5'), and Z54386 (H.sapiens CpG island DNA genomic MseI fragment, clone 10g3, forward read cpg10g3.ft1a). The predicted amino acid sequence disclosed herein for dd119_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd119_4 protein demonstrated at least some similarity to sequences identified as AB011135 (KIAA0563 protein [Homo sapiens]) and M86526 (proline-rich protein [Rattus norvegicus]). The rat proline-rich protein (PRP) is encoded by a single-copy gene and is expressed in the ventral prostate of the rat, with the precursor protein product being cleaved into multiple proline-rich polypeptides. Based upon sequence similarity, dd119_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the dd119_4 protein sequence centered around amino acid 928 of SEQ ID NO:108.

dd119_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 166 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "df202_3"

A polynucleotide of the present invention has been identified as clone "df202_3". df202_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. df202_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "df202_3 protein").

The nucleotide sequence of df202_3 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the df202_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110.

5 Amino acids 17 to 29 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the df202_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone df202_3 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for df202_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. df202_3 demonstrated at least some similarity with sequences
15 identified as AA138679 (mq76g03.r1 Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 584692 5'), AA283121 (zt17b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713361 3'), AA286996 (zs58c10.r1 NCI_CGAP_GCB1 Soares NbHTGBC Homo sapiens cDNA clone IMAGE 701682 5'), N54968 (yv38g01.s1 Homo sapiens cDNA clone 245040 3'), T20071 (Human gene signature HUMGS01213), and
20 W28275 (44g12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA).

The predicted amino acid sequence disclosed herein for df202_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted df202_3 protein demonstrated at least some similarity to the sequence identified as Z81137 (W02D9.h [Caenorhabditis elegans]). Based upon sequence
25 similarity, df202_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the df202_3 protein sequence, centered around amino acids 55, 80, and 108 of SEQ ID NO:110, respectively.

30 Clone "km225_1"

A polynucleotide of the present invention has been identified as clone "km225_1". km225_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. km225_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "km225_1 protein").

5 The nucleotide sequence of km225_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the km225_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the
10 predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the km225_1 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone km225_1 should be approximately 2300 bp.

20 The nucleotide sequence disclosed herein for km225_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. km225_1 demonstrated at least some similarity with sequences identified as AA101603 (zk94h09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490529 3' similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, km225_1 proteins and each similar protein or peptide may share at least some activity.

Clone "mj301_1"

25 A polynucleotide of the present invention has been identified as clone "mj301_1". mj301_1 was isolated from a human adult lymph node cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mj301_1 is a full-length clone,
30 including the entire coding sequence of a secreted protein (also referred to herein as "mj301_1 protein").

 The nucleotide sequence of mj301_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mj301_1 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 65 to 77 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 78. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the mj301_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mj301_1 should be approximately 2760 bp; however, a band of 550 bp has been detected in restriction digests, possibly due to an internal EcoRI or NotI restriction site in the clone.

The nucleotide sequence disclosed herein for mj301_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mj301_1 demonstrated at least some similarity with sequences identified as AA053085 (zl73d01.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510241 3'), AA347293 (EST53566 Fetal heart II Homo sapiens cDNA 5' end), AA813287 (ai76a07.s1 Soares testis NHT Homo sapiens cDNA clone 1376724 3', mRNA sequence), R45713 (Ha117-f Homo sapiens cDNA clone a117-f), T20114 (Human gene signature HUMGS01258), U46278 (Human clone xs252 mRNA sequence), Z36823 (H.sapiens (xs170) mRNA), and Z36832 (H.sapiens (xs170) mRNA). The human xs170 sequence is differentially expressed in pancreatic cancer cells. The predicted amino acid sequence disclosed herein for mj301_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mj301_1 protein demonstrated at least some similarity to the sequence identified as U07818 (putative phospho-beta-glucosidase [Bacillus stearothermophilus]). Based upon sequence similarity, mj301_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the mj301_1 protein sequence centered around amino acid 60 of SEQ ID NO:114.

Clone "ml10_7"

A polynucleotide of the present invention has been identified as clone "ml10_7". ml10_7 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. ml10_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml10_7 protein").

5 The nucleotide sequence of ml10_7 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml10_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 30 to 42 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the
10 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml10_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml10_7 should be approximately 1600 bp.

15 The nucleotide sequence disclosed herein for ml10_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml10_7 demonstrated at least some similarity with sequences identified as AA411457 (zv30f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 3'), AA411585 (zv30f06.r1 Soares ovary tumor NbHOT Homo sapiens
20 cDNA clone 755171 5', mRNA sequence), AA485512 (zx90b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810987 5'), R97588 (yq59b05.r1 Homo sapiens cDNA clone 200049 5' similar to contains MSR1 repetitive element), and T23020 (Human gene signature HUMGS04748). The predicted amino acid sequence disclosed herein for ml10_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the
25 BLASTX search protocol. The predicted ml10_7 protein demonstrated at least some similarity to the sequence identified as R56978 (Human myotonic dystrophy gene protein). Based upon sequence similarity, ml10_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the ml10_7 protein sequence, centered
30 approximately around amino acids 20, 55 (between residues 50 and 60), 85 (between residues 80 and 89), and 175 (between residues 169 and 180) of SEQ ID NO:116, respectively. ml10_7 appears to represent one member of a group of multiple alternatively spliced transcripts.

Clone "my340_1"

A polynucleotide of the present invention has been identified as clone "my340_1". my340_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. my340_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "my340_1 protein").

The nucleotide sequence of my340_1 as presently determined is reported in SEQ
10 ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the my340_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone my340_1 should be approximately 1800 bp.

15 The nucleotide sequence disclosed herein for my340_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. my340_1 demonstrated at least some similarity with sequences identified as AA469015 (nc79g10.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:783618), H85290 (yv86f01.r1 Homo sapiens cDNA clone 249625 5'), L29074
20 (Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds), M86699 (Human kinase (TTK) mRNA, complete cds), W19755 (zb38f08.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305895 5'), W63667 (zc57h10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326467 5', mRNA sequence), and Z84478 (Human DNA sequence). The predicted amino
25 acid sequence disclosed herein for my340_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted my340_1 protein demonstrated at least some similarity to the sequence identified as M86699 (kinase [Homo sapiens]). The human TTK kinase can phosphorylate serine, threonine, and tyrosine hydroxyamino acids. Based upon sequence similarity,
30 my340_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the my340_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

Deposit of Clones

Clones bn365_53, bo342_2, dn721_8, dn834_1, pd278_5, pe80_1, pm113_1, pm749_8, pt31_4, and pv296_5 were deposited on May 7, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)
5 as an original deposit under the Budapest Treaty and were given the accession number ATCC 98752, from which each clone comprising a particular polynucleotide is obtainable.

Clones er311_20, fh149_12, pc201_6, pl87_1, and pm514_4 were deposited on June 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty
10 and were given the accession number ATCC 98781, from which each clone comprising a particular polynucleotide is obtainable.

Clones co155_12, fn189_13, lv2_47, ml243_1, pm96_9, pu261_1, pw214_15, qb56_19, qc646_1, qf116_2, and qf662_3 were deposited on July 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession
15 number ATCC 98808, from which each clone comprising a particular polynucleotide is obtainable.

Clones am748_5, cj507_1, cn922_5, cw691_11, cw1000_2, cw1640_1, d24_1, dd426_1, and di393_2 were deposited on July 16, 1998 with the American Type Culture
20 Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98817, from which each clone comprising a particular polynucleotide is obtainable.

Clones dj167_2, dw665_4, dx146_12, dx219_13, fm3_1, h225_1, kj320_1, ml236_5, and pu282_10, were deposited on July 16, 1998 with the American Type Culture
25 Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98818, from which each clone comprising a particular polynucleotide is obtainable.

Clones at94_2, bf169_13, bl152_12, bz578_1, cb123_1, ch245_1, cj378_3, cw1481_1, dd119_4, df202_3, km225_1, mj301_1, ml10_7, and my340_1 were deposited on July 22,
30 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98822, from which each clone comprising a particular polynucleotide is obtainable.

Clone dj167_19 was deposited on February 5, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207090, from which the dj167_19 clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in the composite deposits above. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

Clone

bn365_53

Probe Sequence

SEQ ID NO:119

	bo342_2	SEQ ID NO:120
	dn721_8	SEQ ID NO:121
	dn834_1	SEQ ID NO:122
	pd278_5	SEQ ID NO:123
5	pe80_1	SEQ ID NO:124
	pm113_1	SEQ ID NO:125
	pm749_8	SEQ ID NO:126
	pt31_4	SEQ ID NO:127
	pv296_5	SEQ ID NO:128
10	er311_20	SEQ ID NO:129
	fh149_12	SEQ ID NO:130
	pc201_6	SEQ ID NO:131
	pl87_1	SEQ ID NO:132
	pm514_4	SEQ ID NO:133
15	co155_12	SEQ ID NO:134
	fn189_13	SEQ ID NO:135
	lv2_47	SEQ ID NO:136
	ml243_1	SEQ ID NO:137
	pm96_9	SEQ ID NO:138
20	pu261_1	SEQ ID NO:139
	pw214_15	SEQ ID NO:140
	qb56_19	SEQ ID NO:141
	qc646_1	SEQ ID NO:142
	qf116_2	SEQ ID NO:143
25	qf662_3	SEQ ID NO:144
	am748_5	SEQ ID NO:145
	cj507_1	SEQ ID NO:146
	cn922_5	SEQ ID NO:147
	cw691_11	SEQ ID NO:148
30	cw1000_2	SEQ ID NO:149
	cw1640_1	SEQ ID NO:150
	d24_1	SEQ ID NO:151
	dd426_1	SEQ ID NO:152
	di393_2	SEQ ID NO:153

	dj167_2	SEQ ID NO:154
	dw665_4	SEQ ID NO:155
	dx146_12	SEQ ID NO:156
	dx219_13	SEQ ID NO:157
5	fm3_1	SEQ ID NO:158
	h225_1	SEQ ID NO:159
	kj320_1	SEQ ID NO:160
	ml236_5	SEQ ID NO:161
	pu282_10	SEQ ID NO:162
10	at94_2	SEQ ID NO:163
	bf169_13	SEQ ID NO:164
	bl152_12	SEQ ID NO:165
	bz578_1	SEQ ID NO:166
	cb123_1	SEQ ID NO:167
15	ch245_1	SEQ ID NO:168
	cj378_3	SEQ ID NO:169
	cw1481_1	SEQ ID NO:170
	dd119_4	SEQ ID NO:171
	df202_3	SEQ ID NO:172
20	km225_1	SEQ ID NO:173
	mj301_1	SEQ ID NO:174
	ml10_7	SEQ ID NO:175
	my340_1	SEQ ID NO:176

25 In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

30 The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

5 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as
10 immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a
15 decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length
20 polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that
25 are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can
30 be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that

has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately
5 labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public
10 databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the
15 polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to
20 identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The
25 desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have
30 multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein).
In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of

transposable elements (Plasterk, 1992, *Bioessays* **14**(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST

version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or

polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

5 The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T _R *; 4xSSC	T _R *; 4xSSC

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,
5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an
15 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably
20 linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies
10 or vectors suitable for introduction of DNA).

Research Uses and Utilities

 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as
10 described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15 Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.
20 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from
25 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and
30 murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2

microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated
5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated
10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without
15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,
20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al.,
25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*
30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;
- 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others,
- 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;
- 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25

Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell
- 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

20 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenberg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

30

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic
5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another
10 material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a
15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the
20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other
25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,
30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

5 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to
10 present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the
15 invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers
20 in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein
25 by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing,
30 prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If
10 administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of
5 antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the
10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing
15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be
20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide
25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful
30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of
10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

5 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

10 Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:1;
 - (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
 - (c) the nucleotide sequence of the full-length protein coding sequence of clone bn365_53 deposited under accession number ATCC 98752;
 - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;
 - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
 - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
 - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:1.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

- (a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and
 - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752.
9. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bn365_53 deposited under accession number ATCC 98752;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:3;
 - (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
 - (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915;

(d) the nucleotide sequence of the full-length protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;

(f) the nucleotide sequence of a mature protein coding sequence of clone bo342_2 deposited under accession number ATCC 98752;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo342_2 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:5;

- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;
 - (c) the nucleotide sequence of the full-length protein coding sequence of clone dn721_8 deposited under accession number ATCC 98752;
 - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;
 - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
 - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
 - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
 - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:5.
15. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dn721_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.
16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:7;
 - (b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;

- (c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dn834_1 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dn834_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:9;
- (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;

(d) the nucleotide sequence of the full-length protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

(f) the nucleotide sequence of a mature protein coding sequence of clone pd278_5 deposited under accession number ATCC 98752;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone pd278_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pe80_1 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pe80_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;

- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
 - (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752;
 - (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone pm113_1 deposited under accession number ATCC 98752;
 - (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
 - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.
23. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm113_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm749_8 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm749_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:17;
- (b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;
- (c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pt31_4 deposited under accession number ATCC 98752;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone pt31_4 deposited under accession number ATCC 98752;
the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pv296_5 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pv296_5 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone er311_20 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone er311_20 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fh149_12 deposited under accession number ATCC 98781;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone fh149_12 deposited under accession number ATCC 98781; the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:25;
- (b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;
- (c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pc201_6 deposited under accession number ATCC 98781;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pc201_6 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pl87_1 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone pl87_1 deposited under accession number ATCC 98781; the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm514_4 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm514_4 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;
- (c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone co155_12 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone co155_12 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;

- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone co155_12 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fn189_13 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fn189_13 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557;
- (c) the nucleotide sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone lv2_47 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
 - (b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;
 - (c) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone lv2_47 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499;
- (c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml243_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ml243_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm96_9 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pm96_9 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pu261_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone pu261_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:43;
- (b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pw214_15 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone pw214_15 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

(b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;

(c) the nucleotide sequence of the full-length protein coding sequence of clone qb56_19 deposited under accession number ATCC 98808;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qb56_19 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;
- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qc646_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qc646_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone qf116_2 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qf116_2 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qf662_3 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone qf662_3 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;
- (c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone am748_5 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone am748_5 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone am748_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cj507_1 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone cj507_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cn922_5 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone cn922_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:59;

(b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cw691_11 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw691_11 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;
- (c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone cw1000_2 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;

- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1000_2 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:63;
- (b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;
- (c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;

- (f) the nucleotide sequence of a mature protein coding sequence of clone cw1640_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1640_1 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone d24_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone d24_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone d24_1 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;

- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dd426_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dd426_1 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone di393_2 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone di393_2 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone di393_2 deposited under accession number ATCC 98817; the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:71;
- (b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dj167_2 deposited under accession number ATCC 98818;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dj167_2 deposited under accession number ATCC 98818; the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:73;
- (b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;
- (c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490;
- (d) the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone dj167_19 deposited under accession number ATCC 207090;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;
- (g) the nucleotide sequence of a mature protein coding sequence of clone dj167_19 deposited under accession number ATCC 207090;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;

- (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
 - (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone dj167_19 deposited under accession number ATCC 207090;
- the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- (c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dw665_4 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dw665_4 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dw665_4 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:77;
- (b) the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dx146_12 deposited under accession number ATCC 98818;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:77.

87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dx146_12 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dx219_13 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dx219_13 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:81;
- (b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;
- (c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fm3_1 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone fm3_1 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone h225_1 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone h225_1 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:84;

(b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and

(c) the amino acid sequence encoded by the cDNA insert of clone h225_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:85;

(b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;

(c) the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;

(d) the nucleotide sequence of the full-length protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;

(f) the nucleotide sequence of a mature protein coding sequence of clone kj320_1 deposited under accession number ATCC 98818;

- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone kj320_1 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:87;
- (b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;
- (c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml236_5 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ml236_5 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:89;
- (b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;

(c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452;

(d) the nucleotide sequence of the full-length protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;

(f) the nucleotide sequence of a mature protein coding sequence of clone pu282_10 deposited under accession number ATCC 98818;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:90;

(b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and

(c) the amino acid sequence encoded by the cDNA insert of clone pu282_10 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;
- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- (c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone at94_2 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone at94_2 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone at94_2 deposited under accession number ATCC 98822; the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:93;
- (b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bf169_13 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bf169_13 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bl152_12 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bl152_12 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:97;
- (b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bz578_1 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone bz578_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:99;

- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;
- (c) the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone cb123_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cb123_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ch245_1 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ch245_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:103;

- (b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone cj378_3 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cj378_3 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;

- (c) the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cw1481_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cw1481_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:107;
- (b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;

- (c) the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dd119_4 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone dd119_4 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;
- (c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone df202_3 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone df202_3 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone df202_3 deposited under accession number ATCC 98822; the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:111;
- (b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- (c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone km225_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone km225_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone km225_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone mj301_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- (c) the amino acid sequence encoded by the cDNA insert of clone mj301_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:115;
- (b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;
- (c) the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml10_7 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone ml10_7 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:117;

(b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;

(c) the nucleotide sequence of the full-length protein coding sequence of clone my340_1 deposited under accession number ATCC 98822;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

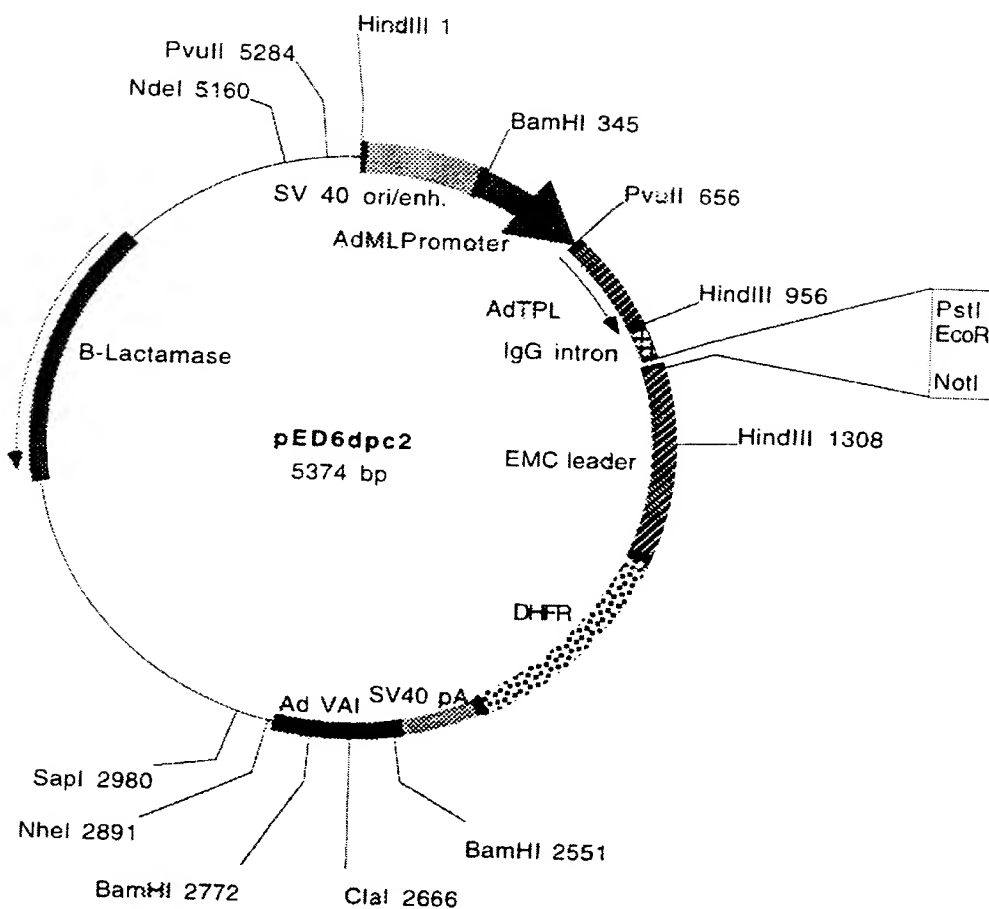
(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone my340_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

FIGURE 1A

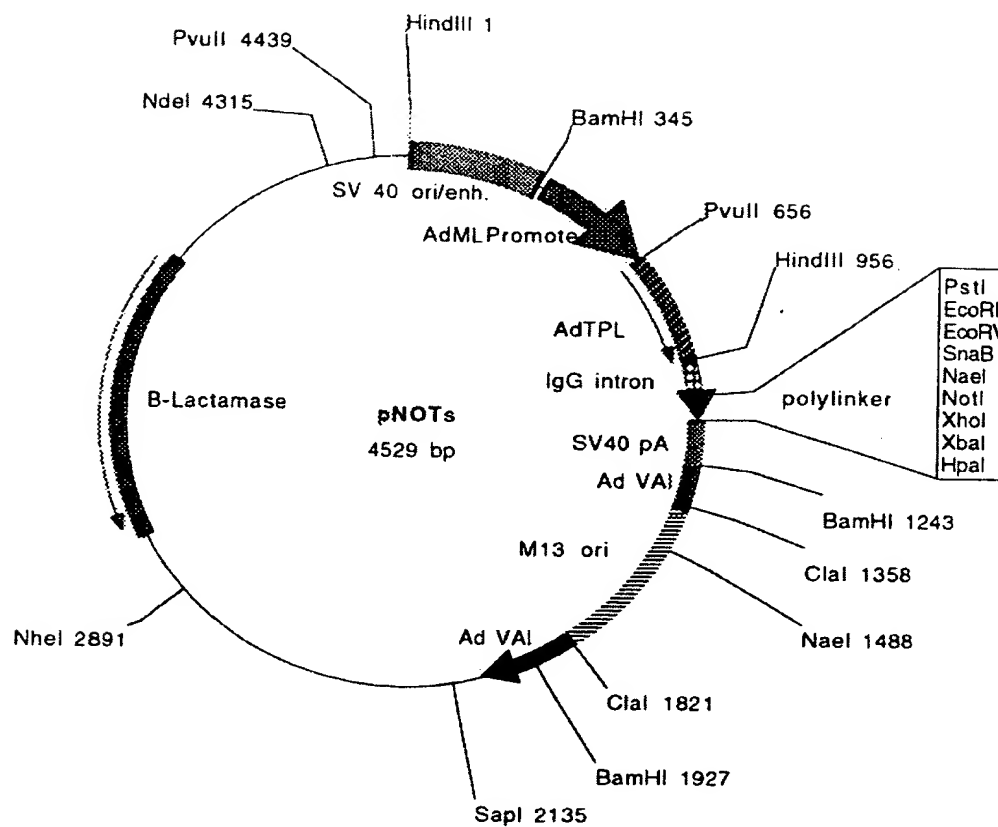


Plasmid name: pED6dpc2

Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs

Plasmid size: 4529 bp

Comments/References: pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the Clal site. SST cDNAs are cloned between EcoRI and NotI

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<110> Jacobs, Kenneth
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 Collins-Racie, Lisa A.
 Evans, Cheryl
 Merberg, David
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 Agostino, Michael J.
 Steininger II, Robert J.
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<210> 6

<211> 647

<212> PRT

<213> Homo sapiens

<400> 6

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Leu Pro Val Asn Val Thr Val Pro Ser Pro Pro Pro Arg Asn Pro Tyr
          20           25           30

Asp Leu His Phe Ile Arg Glu Gly His Arg Tyr Lys Phe Val Asn Ile
  35           40           45

Gln Thr Lys Thr Val Val Val Cys Cys Val Leu Arg Asp Asn Lys Ile
  50           55           60

Leu Pro Met His Phe Pro Leu His Leu Thr Val Pro Lys Phe Ser Leu
  65           70           75           80

Pro Glu His Leu Val Lys Gly Glu Ser Trp Pro Glu Thr Leu Val His
          85           90           95

His Trp Leu Gly Ile Cys Gln Glu Gln Phe Asp Ile Asp Glu Tyr Ser
 100           105           110

Arg Ala Val Arg Asp Val Lys Thr Asp Trp Asn Glu Glu Cys Lys Ser
 115           120           125

Pro Lys Lys Gly Arg Cys Ser Gly His Asn His Val Pro Asn Ser Leu
 130           135           140

Ser Tyr Ala Arg Asp Glu Leu Thr Gln Ser Phe His Arg Leu Ser Val
 145           150           155           160

Cys Val Tyr Gly Asn Asn Leu His Gly Asn Ser Glu Val Asn Leu His
          165           170           175

Gly Cys Arg Asp Leu Gly Gly Asp Trp Ala Pro Phe Pro His Asp Ile
          180           185           190

Leu Pro Tyr Gln Asp Ser Gly Asp Ser Gly Ser Asp Tyr Leu Phe Pro
 195           200           205

Glu Ala Ser Glu Glu Ser Ala Gly Ile Pro Gly Lys Ser Glu Leu Pro
 210           215           220

Tyr Glu Glu Leu Trp Leu Glu Glu Gly Lys Pro Ser His Gln Pro Leu
 225           230           235           240

Thr Arg Ser Leu Ser Glu Lys Asn Arg Cys Asp Gln Phe Arg Gly Ser
          245           250           255

Val Arg Ser Lys Cys Ala Thr Ser Pro Leu Pro Ile Pro Gly Thr Leu
          260           265           270

Gly Ala Ala Val Lys Ser Ser Asp Thr Ala Leu Pro Pro Pro Pro Val
 275           280           285

Pro Pro Lys Ser Glu Ala Val Arg Glu Glu Cys Arg Leu Leu Asn Ala

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290	295	300
Pro Pro Val Pro Pro Arg Ser Ala Lys Pro Leu Ser Thr Ser Pro Ser		
305	310	315 320
Ile Pro Pro Arg Thr Val Lys Pro Ala Arg Gln Gln Thr Arg Ser Pro		
	325	330 335
Ser Pro Thr Leu Ser Tyr Tyr Ser Ser Gly Leu His Asn Ile Val Thr		
	340	345 350
Lys Thr Asp Thr Asn Pro Ser Glu Ser Thr Pro Val Ser Cys Tyr Pro		
	355	360 365
Cys Asn Arg Val Lys Thr Asp Ser Val Asp Leu Lys Ser Pro Phe Gly		
	370	375 380
Ser Pro Ser Ala Glu Ala Val Ser Ser Arg Leu Ser Trp Pro Asn His		
	385	390 395 400
Tyr Ser Gly Ala Ser Glu Ser Gln Thr Arg Ser Asp Phe Leu Leu Asp		
	405	410 415
Pro Ser Arg Ser Tyr Ser Tyr Pro Arg Gln Lys Thr Pro Gly Thr Pro		
	420	425 430
Lys Arg Asn Cys Pro Ala Pro Phe Asp Phe Asp Gly Cys Glu Leu Leu		
	435	440 445
Ala Ser Pro Thr Ser Pro Val Thr Ala Glu Phe Ser Ser Ser Val Ser		
	450	455 460
Gly Cys Pro Lys Ser Ala Ser Tyr Ser Leu Glu Ser Thr Asp Val Lys		
	465	470 475 480
Ser Leu Ala Ala Gly Val Thr Lys Gln Ser Thr Ser Cys Pro Ala Leu		
	485	490 495
Pro Pro Arg Ala Pro Lys Leu Val Glu Glu Lys Val Ala Ser Glu Thr		
	500	505 510
Ser Pro Leu Pro Leu Lys Ile Asp Gly Ala Glu Glu Asp Pro Lys Ser		
	515	520 525
Gly Ser Pro Asp Leu Ser Glu Asp Gln Tyr Phe Val Lys Lys Gly Met		
	530	535 540
Gln Asp Ile Phe Ser Ala Ser Tyr Pro Phe Ser Ser Pro Leu His Leu		
	545	550 555 560
Gln Leu Ala Pro Arg Ser Cys Gly Asp Gly Ser Pro Trp Gln Pro Pro		
	565	570 575
Ala Asp Leu Ser Gly Leu Ser Ile Glu Glu Val Ser Lys Ser Leu Arg		
	580	585 590
Phe Ile Gly Leu Ser Glu Asp Val Ile Ser Phe Phe Val Thr Glu Lys		
	595	600 605
Ile Asp Gly Asn Leu Leu Val Gln Leu Thr Glu Glu Ile Leu Ser Glu		

610

615

620

Asp Phe Lys Leu Ser Lys Leu Gln Val Lys Lys Ile Met Gln Phe Ile
 625 630 635 640

Asn Gly Trp Arg Pro Lys Ile
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<210> 7

<211> 892

<212> DNA

<213> Homo sapiens

<400> 7

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<210> 8

<211> 155

<212> PRT

<213> Homo sapiens

<400> 8

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Met Ala Thr Arg Asn Pro Pro Pro Gln Asp Tyr Glu Ser Asp Asp Asp
  1             5             10             15

Ser Tyr Glu Val Leu Asp Leu Thr Glu Tyr Ala Arg Arg His Gln Trp
      20             25             30

Trp Asn Arg Val Phe Gly His Ser Ser Gly Pro Met Val Glu Lys Tyr
      35             40             45

Ser Val Ala Thr Gln Ile Val Met Gly Gly Val Thr Gly Trp Cys Ala
      50             55             60

Gly Phe Leu Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly
      65             70             75             80

Gly Gly Phe Leu Leu Leu Gln Ile Ala Ser His Ser Gly Tyr Val Gln
      85             90             95

Ile Asp Trp Lys Arg Val Glu Lys Asp Val Asn Lys Ala Lys Arg Gln
      100            105            110

Ile Lys Lys Arg Ala Asn Lys Ala Ala Pro Glu Ile Asn Asn Leu Ile
      115            120            125

```

Glu Glu Ala Thr Glu Phe Ile Lys Gln Asn Ile Val Ile Ser Ser Gly
 130 135 140

Phe Val Gly Gly Phe Leu Leu Gly Leu Ala Ser
 145 150 155

<210> 9

<211> 1850

<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 206

<212> PRT

<213> Homo sapiens

<400> 10

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Met Ala Leu Gly Leu Cys Arg Cys Phe His Pro Arg His Ser Met Ala
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Ala Phe Gly Leu Phe Pro Ala Leu Pro Ser Ala Leu Asn Ser His Pro
  20           25           30

Ala Cys Thr Cys Leu Leu Asp Pro Ser Thr Trp Arg Pro Ala His Val
  35           40           45

```

Ser Gly Pro Ala Leu Ala Ser Ser Pro Gln Ile Leu Ser Val Phe Ser
 50 55 60
 Leu Gly Phe Pro Gly Phe Val Asn Gly Ser Cys Val Ser Arg Tyr Lys
 65 70 75 80
 Pro Asp Ile Ile Ser Pro Pro Gly Leu Pro Pro Pro Asp Leu Pro Ser
 85 90 95
 Ser Val Ser Ile Phe Tyr Leu Gln Leu Leu Cys Ser His Gly His Cys
 100 105 110
 Cys Ile Thr Glu Ser Gly Pro Leu Leu Ser Phe Ser Asn Trp Pro Pro
 115 120 125
 Ser Leu Val Pro His Phe Leu Lys Ser Pro Val His Cys His Gln Ile
 130 135 140
 Lys Leu Ser Pro Ala Arg Ser Pro Leu Ser Glu Lys Pro Pro Leu Thr
 145 150 155 160
 Trp Lys His His Cys Leu Ala His Ile Leu Thr Tyr Ser Pro Ser Arg
 165 170 175
 Leu Asp Pro His Thr Ser Phe Gln Pro Pro Leu Pro Leu His Ser Leu
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 Leu Pro Pro Pro Pro Pro His Pro Leu Val Ser Pro Pro Leu
 195 200 205

<210> 11

<211> 2216

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 126

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Phe Ser Lys His Ser Phe Phe Thr Leu Leu Cys Gly Leu Asp
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Pro Ser Arg Asn Leu Leu Ile Gly Lys Arg Leu Gln Thr Pro Ala Val
          20                      25                      30

Cys Val Leu Gln Val His Ala Ala Lys Val Ile Pro Ala His Pro Cys
          35                      40                      45

Pro Val Ser Val Ser Phe Arg Val Ile Pro Tyr Leu Ser Ile Gly Gly
          50                      55                      60

Leu Ile Leu Leu Asp Phe Leu Lys Thr Leu Arg Trp Ser Ile Arg Ser
          65                      70                      75                      80

Asp Phe Ser His Ser Ser Ala Gly Glu Leu Arg Ile Thr Ser Ser Phe
          85                      90                      95

Gly Arg Trp Ser Trp Val Arg Gly Ser Trp Tyr Thr Val Phe Ile Val
          100                      105                      110

Ser Leu Ile Gln Asn Ala Asn Lys Phe Asn Val Phe Leu Pro
          115                      120                      125

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<210> 13

<211> 1426

<212> DNA

<213> Homo sapiens

<400> 13

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<210> 14

<211> 80

<212> PRT

<213> Homo sapiens

<400> 14

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Met Pro Pro Leu Val Ser Pro Gln Cys Ala Pro Ala His Pro Gly Ser
  1                      5                      10                      15

```

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Ala Leu Ser Asp Pro Cys Thr Pro Leu Met Ser Pro Arg Arg Ala Ser
          20                      25                      30

```

```

Cys Ser Ser Pro Ser Ile Tyr Leu Ser Leu Ser Leu Leu Val Gly His
          35                      40                      45

```

```

Phe Val Cys Arg Ala Val Glu Asn Arg Thr Ser Glu Leu Asn Ile Cys
          50                      55                      60

```

```

Pro Asp Val Lys Val Leu Phe Met Thr Thr Leu Leu Ser Met Tyr Met
          65                      70                      75                      80

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<210> 15

<211> 2364

<212> DNA

<213> Homo sapiens

<400> 15

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2364

<210> 16

<211> 463

<212> PRT

<213> Homo sapiens

<400> 16

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Met Ser Gly Gly Thr Pro Tyr Ile Gly Ser Lys Ile Ser Leu Ile Ser
  1             5             10             15

```

```

Lys Ala Glu Ile Arg Tyr Glu Gly Ile Leu Tyr Thr Ile Asp Thr Glu
      20             25             30

```

```

Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp
      35             40             45

```

```

Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr
      50             55             60

```

```

Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro
      65             70             75             80

```

```

Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser
      85             90             95

```

```

Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly
      100            105            110

```

```

Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe Ser Pro Ser Ser Leu
      115            120            125

```

```

Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr
      130            135            140

```

Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr Leu Pro Gln Ser Ser
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 Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg Ser Leu Lys Thr Gln
 165 170 175
 Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp Pro Leu Arg Lys Ser
 180 185 190
 Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser Ala His Leu Pro Ala
 195 200 205
 Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser Thr Arg Pro Leu Pro
 210 215 220
 Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu His Arg Gln Ala Glu
 225 230 235 240
 Val His Lys Val Ser Arg Pro Glu Asn Glu Gln Leu Arg Asn Asp Asn
 245 250 255
 Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala Pro Arg Arg Gly Arg
 260 265 270
 Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly Ile Arg Arg Asp Gly
 275 280 285
 Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu Ser Ala Asn Ala Gln
 290 295 300
 Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His Asn Lys Leu Lys Leu
 305 310 315 320
 Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro Val Asn Gly Glu Asp
 325 330 335
 Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser Glu Gly Asn Ala Asp
 340 345 350
 Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr Asp Lys Thr Lys Ser
 355 360 365
 Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg Glu Arg Arg Pro Thr
 370 375 380
 Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr Phe Gly Ile Pro Leu
 385 390 395 400
 Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Leu Gly
 405 410 415
 Phe Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Thr Phe Thr
 420 425 430
 Ala Pro Arg Gly Phe Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Arg
 435 440 445
 Glu Phe Ala Asp Phe Glu Tyr Arg Lys Thr Thr Ala Phe Gly Pro
 450 455 460

<210> 17
 <211> 2760
 <212> DNA
 <213> Homo sapiens

<400> 17
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<210> 18
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 18

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 Ser Pro Arg Val Gln Arg Gln Val Thr Ser Leu Leu Arg Arg Val Leu
 35 40 45
 Pro Glu Val Thr Pro Ser Arg Leu Ala Ser Ile Ile Gly Val Lys Ser
 50 55 60
 Leu Pro Pro Ala Asp Ile Ser Asp Ile Ile His Ser Thr Glu Lys Gly
 65 70 75 80
 Asp Trp Asn Lys Leu Gly Ile Leu Asp Met Phe Leu Gly Cys Ile Ala
 85 90 95
 Lys Ala Leu Thr Val Gln Leu Lys Ala Lys Gly Thr Thr Ile Thr Gly
 100 105 110
 Thr Ala Gly Thr Thr Val Gly Lys Gly Val Thr Thr Val Thr Leu Pro
 115 120 125
 Met Ile Phe Asn Ser Ser Tyr Leu Arg Arg Gly Glu Ser His Trp Trp
 130 135 140
 Met Lys Gly Ser Thr Pro Thr Gln Ile Ser Glu Ile Ile Ile Lys Leu
 145 150 155 160
 Ile Lys Asp Met Ala Ala Gly His Leu Ser Glu Ala Trp Ser Arg Val
 165 170 175
 Thr Lys Asn Ala Ile Ala Glu Thr Ile Ile Ala Leu Thr Lys Met Glu
 180 185 190
 Glu Glu Phe Arg Ser Pro Val Arg Cys Ile Ala Thr Thr Arg Leu Trp
 195 200 205
 Leu Ala Leu Ala Ser Leu Cys Val Leu Asp Gln Asp His Val Asp Arg
 210 215 220
 Leu Ser Ser Gly Arg Trp Met Gly Lys Asp Gly Gln Gln Lys Gln Met
 225 230 235 240
 Pro Met Cys Asp Asn His Asp Asp Gly Glu Thr Ala Ala Ile Ile Leu
 245 250 255
 Cys Asn Val Cys Gly Asn Leu Cys Thr Asp Cys Asp Arg Phe Leu His
 260 265 270
 Leu His Arg Arg Thr Lys Thr His Gln Arg Gln Val Phe Lys Glu Glu
 275 280 285
 Glu Glu Ala Ile Lys Val Asp Leu His Glu Gly Cys Gly Arg Thr Lys
 290 295 300
 Leu Phe Trp Leu Met Ala Leu Ala Asp Ser Lys Thr Met Lys Ala Met
 305 310 315 320

Val Glu Phe Arg Glu His Thr Gly Lys Pro Thr Thr Ser Ser Ser Glu
 325 330 335
 Ala Cys Arg Phe Cys Gly Ser Arg Ser Gly Thr Glu Leu Ser Ala Val
 340 345 350
 Gly Ser Val Cys Ser Asp Ala Asp Cys Gln Glu Tyr Ala Lys Ile Ala
 355 360 365
 Cys Ser Lys Thr His Pro Cys Gly His Pro Cys Gly Gly Val Lys Asn
 370 375 380
 Glu Glu His Cys Leu Pro Cys Leu His Gly Cys Asp Lys Ser Ala Thr
 385 390 395 400
 Ser Leu Lys Gln Asp Ala Asp Asp Met Cys Met Ile Cys Phe Thr Glu
 405 410 415
 Ala Leu Ser Ala Ala Pro Ala Ile Gln Leu Asp Cys Ser His Ile Phe
 420 425 430
 His Leu Gln Cys Cys Arg Arg Val Leu Glu Asn Arg Trp Leu Gly Pro
 435 440 445
 Arg Ile Thr Phe Gly Phe Ile Ser Cys Pro Ile Cys Lys Asn Lys Ile
 450 455 460
 Asn His Ile Val Leu Lys Asp Leu Leu Asp Pro Ile Lys Glu Leu Tyr
 465 470 475 480
 Glu Asp Val Arg Arg Lys Ala Leu Met Arg Leu Glu Tyr Glu Gly Leu
 485 490 495
 His Lys Ser Glu Ala Ile Thr Thr Pro Gly Val Arg Phe Tyr Asn Asp
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 Pro Ala Gly Tyr Ala Met Asn Arg Tyr Ala Tyr Tyr Val Cys Tyr Lys
 515 520 525
 Cys Arg Lys Ala Tyr Phe Gly Gly Glu Ala Arg Cys Asp Ala Glu Ala
 530 535 540
 Gly Arg Gly Asp Asp Tyr Asp Pro Arg Glu Leu Ile Cys Gly Ala Cys
 545 550 555 560
 Ser Asp Val Ser Arg Ala Gln Met Cys Pro Lys His Gly Thr Asp Phe
 565 570 575
 Leu Glu Tyr Lys Cys Arg Tyr Cys Cys Ser Val Ala Val Phe Phe Cys
 580 585 590
 Phe Gly Thr Thr His Phe Cys Asn Ala Cys His Asp Asp Phe Gln Arg
 595 600 605
 Met Thr Ser Ile Pro Lys Glu Glu Leu Pro His Cys Pro Ala Gly Pro
 610 615 620
 Lys Gly Lys Gln Leu Glu Gly Thr Glu Cys Pro Leu His Val Val His
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Pro Pro Thr Gly Glu Glu Phe Ala Leu Gly Cys Gly Val Cys Arg Asn
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Ala His Thr Phe
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<210> 19

<211> 1649

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20

<211> 92

<212> PRT

<213> Homo sapiens

<400> 20

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Met Gly Glu Pro Ala Gly Gly Glu Asn Pro Pro Leu Ser Pro His Pro
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Pro Gly Arg Ala Asn Val Lys Leu Leu Ile Phe Val Leu Tyr Ile Phe
      20             25             30

Tyr Ile Asn Ile Ser Ile Phe Phe Leu Gln Asn Gln Phe Ile Asn Gly
      35             40             45

Arg Gly Val Trp Gly Gly His Met Glu Leu Pro Leu Trp Gly Gly Pro
      50             55             60

```

Leu His Tyr Pro Thr Tyr Arg Pro Phe Pro His Pro Pro Pro His Ser
 65 70 75 80

Pro Pro Pro Gly Cys Asp Cys Cys Lys Met Gly Val
 85 90

<210> 21
 <211> 2644
 <212> DNA
 <213> Homo sapiens

<400> 21
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<210> 22

<211> 667
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (250)

<400> 22

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Met Ala Asp Ile Leu Ser Gln Ser Glu Thr Leu Ala Ser Gln Asp Leu
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Ser Gly Asp Phe Lys Lys Pro Ala Leu Pro Val Ser Pro Ala Ala Arg
      20              25              30

Ser Lys Ala Pro Ala Ser Ser Ser Ser Asn Pro Glu Glu Val Gln Lys
      35              40              45

Glu Gly Pro Thr Ala Leu Gln Asp Ser Asn Ser Gly Glu Pro Asp Ile
 50              55              60

Pro Pro Pro Gln Pro Asp Cys Gly Asp Phe Arg Ser Leu Gln Glu Glu
 65              70              75              80

Gln Ser Arg Pro Thr Thr Ala Val Ser Ser Pro Gly Gly Pro Ala Arg
      85              90              95

Ala Pro Pro Tyr Gln Glu Pro Pro Trp Gly Gly Pro Ala Thr Ala Pro
      100              105              110

Tyr Ser Leu Glu Thr Leu Lys Gly Gly Thr Ile Leu Gly Thr Arg Ser
      115              120              125

Leu Lys Gly Thr Ser Tyr Cys Leu Phe Gly Arg Leu Ser Gly Cys Asp
      130              135              140

Val Cys Leu Glu His Pro Ser Val Ser Arg Tyr His Ala Val Leu Gln
      145              150              155              160

His Arg Ala Ser Gly Pro Asp Gly Glu Cys Asp Ser Asn Gly Pro Gly
      165              170              175

Phe Tyr Leu Tyr Asp Leu Gly Ser Thr His Gly Thr Phe Leu Asn Lys
      180              185              190

Thr Arg Ile Pro Pro Arg Thr Tyr Cys Arg Val His Val Gly His Val
      195              200              205

Val Arg Phe Gly Gly Ser Thr Arg Leu Phe Ile Leu Gln Gly Pro Glu
      210              215              220

Glu Asp Arg Glu Ala Glu Ser Glu Leu Thr Val Thr Gln Leu Lys Glu
      225              230              235              240

Leu Arg Lys Gln Gln Gln Ile Leu Leu Xaa Lys Lys Met Leu Gly Glu
      245              250              255

Asp Ser Asp Glu Glu Glu Glu Met Asp Thr Ser Glu Arg Lys Ile Asn
      260              265              270

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Ala Gly Ser Gln Asp Asp Glu Met Gly Cys Thr Trp Gly Met Gly Glu
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 Asp Ala Val Glu Asp Asp Ala Glu Glu Asn Pro Ile Val Leu Glu Phe
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 Gln Gln Glu Arg Glu Ala Phe Tyr Ile Lys Asp Pro Lys Lys Ala Leu
 305 310 315 320
 Gln Gly Phe Phe Asp Arg Glu Gly Glu Glu Leu Glu Tyr Glu Phe Asp
 325 330 335
 Glu Gln Gly His Ser Thr Trp Leu Cys Arg Val Arg Leu Pro Val Asp
 340 345 350
 Asp Ser Thr Gly Lys Gln Leu Val Ala Glu Ala Ile His Ser Gly Lys
 355 360 365
 Lys Lys Glu Ala Met Ile Gln Cys Ser Leu Glu Ala Cys Arg Ile Leu
 370 375 380
 Asp Thr Leu Gly Leu Leu Arg Gln Glu Ala Val Ser Arg Lys Arg Lys
 385 390 395 400
 Ala Lys Asn Trp Glu Asp Glu Asp Phe Tyr Asp Ser Asp Asp Asp Thr
 405 410 415
 Phe Leu Asp Arg Thr Gly Leu Ile Glu Lys Lys Arg Leu Asn Arg Met
 420 425 430
 Lys Lys Ala Gly Lys Ile Asp Glu Lys Pro Glu Thr Phe Glu Ser Leu
 435 440 445
 Val Ala Lys Leu Asn Asp Ala Glu Arg Glu Leu Ser Glu Ile Ser Glu
 450 455 460
 Arg Leu Lys Ala Ser Ser Gln Val Leu Ser Glu Ser Pro Ser Gln Asp
 465 470 475 480
 Ser Leu Asp Ala Phe Met Ser Glu Met Lys Ser Gly Ser Thr Leu Asp
 485 490 495
 Gly Val Ser Arg Lys Lys Leu His Leu Arg Thr Phe Glu Leu Arg Lys
 500 505 510
 Glu Gln Gln Arg Leu Lys Gly Leu Ile Lys Ile Val Lys Pro Ala Glu
 515 520 525
 Ile Pro Glu Leu Lys Lys Thr Glu Thr Gln Thr Thr Gly Ala Glu Asn
 530 535 540
 Lys Ala Lys Lys Leu Thr Leu Pro Leu Phe Gly Ala Met Lys Gly Gly
 545 550 555 560
 Ser Lys Phe Lys Leu Lys Thr Gly Thr Val Gly Lys Leu Pro Pro Lys
 565 570 575
 Arg Pro Glu Leu Pro Pro Thr Leu Met Arg Met Lys Asp Glu Pro Glu
 580 585 590

Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Lys Glu
 595 600 605

Glu His Glu Lys Lys Lys Leu Glu Asp Gly Ser Leu Ser Arg Pro Gln
 610 615 620

Pro Glu Ile Glu Pro Glu Ala Ala Val Gln Glu Met Arg Pro Pro Thr
 625 630 635 640

Asp Leu Thr His Phe Lys Glu Thr Gln Thr His Gly Asn Ile Phe Leu
 645 650 655

Leu Leu Pro Val Leu Phe Ser Gly Gln Leu His
 660 665

<210> 23

<211> 2402

<212> DNA

<213> Homo sapiens

<400> 23

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 aa 2402

<210> 24

<211> 520

<212> PRT

<213> Homo sapiens

<400> 24

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 35 40 45
 Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser Gly Phe Ala Pro
 50 55 60
 Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp Tyr Asn Gly Leu Pro
 65 70 75 80
 Val Leu Thr Thr Asn Ala Ile Gly Gln Trp Asp Leu Val Cys Asp Leu
 85 90 95
 Gly Trp Gln Val Ile Leu Glu Gln Ile Leu Phe Ile Leu Gly Phe Ala
 100 105 110
 Ser Gly Tyr Leu Phe Leu Gly Tyr Pro Ala Asp Arg Phe Gly Arg Arg
 115 120 125
 Gly Ile Val Leu Leu Thr Leu Gly Leu Val Gly Pro Cys Gly Val Gly
 130 135 140
 Gly Ala Ala Ala Gly Ser Ser Thr Gly Val Met Ala Leu Arg Phe Leu
 145 150 155 160
 Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg
 165 170 175
 Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly
 180 185 190
 Glu Leu Val Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu
 195 200 205
 Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys
 210 215 220
 Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala
 225 230 235 240
 Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu
 245 250 255
 Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu
 260 265 270

Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro
 275 280 285
 Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu Leu Asn Tyr Arg Asn Ile
 290 295 300
 Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr Asn Phe Ile Ala His Ala
 305 310 315 320
 Ile Arg His Cys Tyr Gln Pro Val Gly Gly Gly Gly Ser Pro Ser Asp
 325 330 335
 Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly Thr Ala Ala Leu Ala Cys
 340 345 350
 Val Phe Leu Gly Val Thr Val Asp Arg Phe Gly Arg Arg Gly Ile Leu
 355 360 365
 Leu Leu Ser Met Thr Leu Thr Gly Ile Ala Ser Leu Val Leu Leu Gly
 370 375 380
 Leu Trp Asp Tyr Leu Asn Glu Ala Ala Ile Thr Thr Phe Ser Val Leu
 385 390 395 400
 Gly Leu Phe Ser Ser Gln Ala Ala Ala Ile Leu Ser Thr Leu Leu Ala
 405 410 415
 Ala Glu Val Ile Pro Thr Thr Val Arg Gly Arg Gly Leu Gly Leu Ile
 420 425 430
 Met Ala Leu Gly Ala Leu Gly Gly Leu Ser Gly Pro Ala Gln Arg Leu
 435 440 445
 His Met Gly His Gly Ala Phe Leu Gln His Val Val Leu Ala Ala Cys
 450 455 460
 Ala Leu Leu Cys Ile Leu Ser Ile Met Leu Leu Pro Glu Thr Lys Arg
 465 470 475 480
 Lys Leu Leu Pro Glu Val Leu Arg Asp Gly Glu Leu Cys Arg Arg Pro
 485 490 495
 Ser Leu Leu Arg Gln Pro Pro Pro Thr Arg Cys Asp His Val Pro Leu
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<210> 25

<211> 2377

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 351

<212> PRT

<213> Homo sapiens

<400> 26

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          20                      25                      30
Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu
          35                      40                      45
Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu
          50                      55                      60
Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys
          65                      70                      75                      80
Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val
          85                      90                      95

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Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu
 100 105 110
 Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu
 115 120 125
 Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His
 130 135 140
 Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro
 145 150 155 160
 Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys
 165 170 175
 Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly
 180 185 190
 His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe
 195 200 205
 Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val
 210 215 220
 Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys
 225 230 235 240
 Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln
 245 250 255
 Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr
 260 265 270
 Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg
 275 280 285
 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe
 290 295 300
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp
 305 310 315 320
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 325 330 335
 Thr Lys Val Ala Lys Leu Lys Ser Gln Ser Gly Tyr Pro Ser Ile
 340 345 350

<210> 27

<211> 460

<212> DNA

<213> Homo sapiens

<400> 27

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 gccctctggc tgcaggcggg gcccaagccct tggtagagag ccgcagtgtg agcctgcgca 240

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accagaaaga taagactgtt cttaacgacc tagatgattc tgttcacatc tgaacgggat 360
cagggttttgt cctcactcca attaaaagaa agcaatgtca catgaaaaaa aaaaaaaaaa 420
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

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460

<210> 28

<211> 85

<212> PRT

<213> Homo sapiens

<400> 28

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Met Lys Pro Ala Val Asp Glu Met Phe Pro Glu Gly Ala Gly Pro Tyr
  1              5              10              15

```

```

Val Asp Leu Asp Glu Ala Gly Gly Ser Thr Gly Leu Leu Met Asp Leu
      20              25              30

```

```

Ala Ala Asn Glu Lys Pro Phe Met Gln Thr Phe Leu Thr Ile Leu Lys
      35              40              45

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Ile Phe Leu Met Met Met Thr Ser Ser Glu Met Pro Ser Gly Cys Arg
      50              55              60

```

```

Arg Gly Gln Ala Leu Gly Thr Glu Pro Gln Cys Glu Pro Ala Gln Asp
      65              70              75              80

```

```

Ser Phe Arg Trp Phe
              85

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<210> 29

<211> 3204

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 741

<212> PRT

<213> Homo sapiens

<400> 30

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Met Ala Glu Pro Val Ser Pro Leu Lys His Phe Val Leu Ala Lys Lys
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```

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Ala Ile Thr Ala Ile Phe Asp Gln Leu Leu Glu Phe Val Thr Glu Gly
      20                      25                      30

```

```

Ser His Phe Val Glu Ala Thr Tyr Lys Asn Pro Glu Leu Asp Arg Ile
      35                      40                      45

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Ala Thr Glu Asp Asp Leu Val Glu Met Gln Gly Tyr Lys Asp Lys Leu
      50                      55                      60

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```

Ser Ile Ile Gly Glu Val Leu Ser Arg Arg His Met Lys Val Ala Phe
      65                      70                      75                      80

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Phe Gly Arg Thr Ser Ser Gly Lys Ser Ser Val Ile Asn Ala Met Leu
      85                      90                      95

```

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Trp Asp Lys Val Leu Pro Ser Gly Ile Gly His Ile Thr Asn Cys Phe
      100                      105                      110

```

```

Leu Ser Val Glu Gly Thr Asp Gly Asp Lys Ala Tyr Leu Met Thr Glu
      115                      120                      125

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Gly Ser Asp Glu Lys Lys Ser Val Lys Thr Val Asn Gln Leu Ala His
 130 135 140
 Ala Leu His Met Asp Lys Asp Leu Lys Ala Gly Cys Leu Val Arg Val
 145 150 155 160
 Phe Trp Pro Lys Ala Lys Cys Ala Leu Leu Arg Asp Asp Leu Val Leu
 165 170 175
 Val Asp Ser Pro Gly Thr Asp Val Thr Thr Glu Leu Asp Ser Trp Ile
 180 185 190
 Asp Lys Phe Cys Leu Asp Ala Asp Val Phe Val Leu Val Ala Asn Ser
 195 200 205
 Glu Ser Thr Leu Met Asn Thr Glu Lys His Phe Phe His Lys Val Asn
 210 215 220
 Glu Arg Leu Ser Lys Pro Asn Ile Phe Ile Leu Asn Asn Arg Trp Asp
 225 230 235 240
 Ala Ser Ala Ser Glu Pro Glu Tyr Met Glu Asp Val Arg Arg Gln His
 245 250 255
 Met Glu Arg Cys Leu His Phe Leu Val Glu Glu Leu Lys Val Val Asn
 260 265 270
 Ala Leu Glu Ala Gln Asn Arg Ile Phe Phe Val Ser Ala Lys Glu Val
 275 280 285
 Leu Ser Ala Arg Lys Gln Lys Ala Gln Gly Met Pro Glu Ser Gly Val
 290 295 300
 Ala Leu Ala Glu Gly Phe His Ala Arg Leu Gln Glu Phe Gln Asn Phe
 305 310 315 320
 Glu Gln Ile Phe Glu Glu Cys Ile Ser Gln Ser Ala Val Lys Thr Lys
 325 330 335
 Phe Glu Gln His Thr Ile Arg Ala Lys Gln Ile Leu Ala Thr Val Lys
 340 345 350
 Asn Ile Met Asp Ser Val Asn Leu Ala Ala Glu Asp Lys Arg His Tyr
 355 360 365
 Ser Val Glu Glu Arg Glu Asp Gln Ile Asp Arg Leu Asp Phe Ile Arg
 370 375 380
 Asn Gln Met Asn Leu Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu
 385 390 395 400
 Val Thr Glu Glu Val Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu
 405 410 415
 Ile Cys Arg Leu Ser Val Leu Val Asp Glu Phe Cys Ser Glu Phe His
 420 425 430
 Pro Asn Pro Asp Val Leu Lys Ile Tyr Lys Ser Glu Leu Asn Lys His
 435 440 445

Ile Glu Asp Gly Met Gly Arg Asn Leu Ala Asp Arg Cys Thr Asp Glu
 450 455 460
 Val Asn Ala Leu Val Pro Gln Thr Gln Gln Glu Ile Ile Glu Asn Leu
 465 470 475 480
 Lys Pro Leu Leu Pro Ala Gly Ile Gln Asp Lys Leu His Thr Leu Ile
 485 490 495
 Pro Cys Lys Lys Phe Asp Leu Ser Tyr Asn Leu Asn Tyr His Lys Leu
 500 505 510
 Cys Ser Asp Phe Gln Glu Asp Ile Val Phe Arg Phe Ser Leu Gly Trp
 515 520 525
 Ser Ser Leu Val His Arg Phe Leu Gly Pro Arg Asn Ala Gln Arg Val
 530 535 540
 Leu Leu Gly Leu Ser Glu Pro Ile Phe Gln Leu Pro Arg Ser Leu Ala
 545 550 555 560
 Ser Thr Pro Thr Ala Pro Thr Thr Pro Ala Thr Pro Asp Asn Ala Ser
 565 570 575
 Gln Glu Glu Leu Met Ile Thr Leu Val Thr Gly Leu Ala Ser Val Thr
 580 585 590
 Ser Arg Thr Ser Met Gly Ile Ile Ile Val Gly Gly Val Ile Trp Lys
 595 600 605
 Thr Ile Gly Trp Lys Leu Leu Ser Val Ser Leu Thr Met Tyr Gly Ala
 610 615 620
 Leu Tyr Leu Tyr Glu Arg Leu Ser Trp Thr Thr His Ala Lys Glu Arg
 625 630 635 640
 Ala Phe Lys Gln Gln Phe Val Asn Tyr Ala Thr Glu Lys Leu Arg Met
 645 650 655
 Ile Val Ser Ser Thr Ser Ala Asn Cys Ser His Gln Val Lys Gln Gln
 660 665 670
 Ile Ala Thr Thr Phe Ala Arg Leu Cys Gln Gln Val Asp Ile Thr Gln
 675 680 685
 Lys Gln Leu Glu Glu Glu Ile Ala Arg Leu Pro Lys Glu Ile Asp Gln
 690 695 700
 Leu Glu Lys Ile Gln Asn Asn Ser Lys Leu Leu Arg Asn Lys Ala Val
 705 710 715 720
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 Ser Asn Glu Asp Ser
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<210> 31

<211> 2483

<212> DNA

<213> Homo sapiens

<400> 31

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2483

<210> 32

<211> 654

<212> PRT

<213> Homo sapiens

<400> 32

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Leu Ala Ser Ser Ser Thr Ala Ala Ala Ala Thr Leu Ser Leu Ala Asn
                20                      25                      30

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Ser Asp Val Ser Leu Leu Asn Tyr Gln Ser Ala Leu Tyr Pro Ser Ser
 35 40 45
 Ala Ala Pro Val Pro Gly Val Ala Gln Gln Gly Val Ser Leu Gln Pro
 50 55 60
 Gly Thr Thr Gln Ile Cys Thr Gln Thr Asp Pro Phe Gln Gln Thr Phe
 65 70 75 80
 Ile Val Cys Pro Pro Ala Phe Gln Thr Gly Leu Gln Ala Thr Thr Lys
 85 90 95
 His Ser Gly Phe Pro Val Arg Met Asp Asn Ala Val Pro Ile Val Pro
 100 105 110
 Gln Ala Pro Ala Ala Gln Pro Thr Thr Asp Ser Val Arg Ser Ser His
 115 120 125
 Ala Asp Leu Gln Gly Lys Asn Ile Gln Thr Phe Leu Arg Asn Gly Leu
 130 135 140
 Leu Arg Lys Leu Tyr Thr Thr Asn Gly Ser Asn Ser Pro Pro Ser Ser
 145 150 155 160
 Ser His Ile Thr Pro Gln Tyr Ala Val Pro Phe Thr Leu Ser Cys Ala
 165 170 175
 Ala Gly Arg Pro Ala Leu Val Glu Gln Thr Ala Ala Val Leu Gln Ala
 180 185 190
 Trp Pro Gly Gly Thr Gln Gln Ile Leu Leu Pro Ser Thr Trp Gln Gln
 195 200 205
 Leu Pro Gly Val Ala Leu His Asn Ser Val Gln Pro Thr Ala Met Ile
 210 215 220
 Pro Glu Ala Met Gly Ser Gly Gln Gln Leu Ala Asp Trp Arg Asn Ala
 225 230 235 240
 His Ser His Gly Asn Gln Tyr Ser Thr Ile Met Gln Gln Pro Ser Leu
 245 250 255
 Leu Thr Asn His Val Thr Leu Ala Thr Ala Gln Pro Leu Asn Val Gly
 260 265 270
 Val Ala His Val Val Arg Gln Gln Gln Ser Ser Ser Leu Pro Ser Lys
 275 280 285
 Lys Asn Lys Gln Ser Ala Pro Val Ser Ser Lys Ser Ser Leu Asp Val
 290 295 300
 Leu Pro Ser Gln Val Tyr Ser Leu Val Gly Ser Ser Pro Leu Arg Thr
 305 310 315 320
 Thr Ser Ser Tyr Asn Ser Leu Val Pro Val Gln Asp Gln His Gln Pro
 325 330 335
 Ile Ile Ile Pro Asp Thr Pro Ser Pro Pro Val Ser Val Ile Thr Ile
 340 345 350

Arg Ser Asp Thr Asp Glu Glu Glu Asp Asn Lys Tyr Lys Pro Ser Ser
 355 360 365
 Ser Gly Leu Lys Pro Arg Ser Asn Val Ile Ser Tyr Val Thr Val Asn
 370 375 380
 Asp Ser Pro Asp Ser Asp Ser Ser Leu Ser Ser Pro Tyr Ser Thr Asp
 385 390 395 400
 Thr Leu Ser Ala Leu Arg Gly Asn Ser Gly Ser Val Leu Glu Gly Pro
 405 410 415
 Gly Arg Val Val Ala Asp Gly Thr Gly Thr Arg Thr Ile Ile Val Pro
 420 425 430
 Pro Leu Lys Thr Gln Leu Gly Asp Cys Thr Val Ala Thr Gln Ala Ser
 435 440 445
 Gly Leu Leu Ser Asn Lys Thr Lys Pro Val Ala Ser Val Ser Gly Gln
 450 455 460
 Ser Ser Gly Cys Cys Ile Thr Pro Thr Gly Tyr Arg Ala Gln Arg Gly
 465 470 475 480
 Gly Thr Ser Ala Ala Gln Pro Leu Asn Leu Ser Gln Asn Gln Gln Ser
 485 490 495
 Ser Ala Ala Pro Thr Ser Gln Glu Arg Ser Ser Asn Pro Ala Pro Arg
 500 505 510
 Arg Gln Gln Ala Phe Val Ala Pro Leu Ser Gln Ala Pro Tyr Thr Phe
 515 520 525
 Gln His Gly Ser Pro Leu His Ser Thr Gly His Pro His Leu Ala Pro
 530 535 540
 Ala Pro Ala His Leu Pro Ser Gln Ala His Leu Tyr Thr Tyr Ala Ala
 545 550 555 560
 Pro Thr Ser Ala Ala Ala Leu Gly Ser Thr Ser Ser Ile Ala His Leu
 565 570 575
 Phe Ser Pro Gln Gly Ser Ser Arg His Ala Ala Ala Tyr Thr Thr His
 580 585 590
 Pro Ser Thr Leu Val His Gln Val Pro Val Ser Val Gly Pro Ser Leu
 595 600 605
 Leu Thr Ser Ala Ser Val Ala Pro Ala Gln Tyr Gln His Gln Phe Ala
 610 615 620
 Thr Gln Ser Tyr Ile Gly Ser Ser Arg Gly Ser Thr Ile Tyr Thr Gly
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<210> 33

<211> 2731

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2173)

<220>

<221> unsure

<222> (2700)

<400> 33

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<210> 34

<211> 441

<212> PRT

<213> Homo sapiens

<400> 34

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Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
  1              5              10              15

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
              20              25              30

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
              35              40              45

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
  50              55              60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
  65              70              75              80

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
              85              90              95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
              100              105              110

Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys
              115              120              125

Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg
              130              135              140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn
              145              150              155              160

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr
              165              170              175

Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser
              180              185              190

Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met
              195              200              205

Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr
              210              215              220

Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe
              225              230              235              240

Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu
              245              250              255

Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu
              260              265              270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg His Lys Gly Glu
              275              280              285

Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys

```


290 295 300
 Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly
 305 310 315 320
 Ile Val Lys Pro Arg Leu Gly Val Thr Leu His Lys Val Val Val Ala
 325 330 335
 Gly Ala Leu Tyr Leu Leu Phe Ser Gly Met Glu Gly Val Leu Arg Val
 340 345 350
 Thr Gly Ala Gln Thr Asp Leu Ala Ser Leu Ala Phe Ile Pro Leu Ala
 355 360 365
 Phe Leu Asp Thr Ala Leu Cys Trp Trp Ile Phe Ile Ser Leu Thr Gln
 370 375 380
 Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu
 385 390 395 400
 Tyr Arg His Phe Thr Asn Thr Leu Ile Leu Ala Val Ala Ala Ser Ile
 405 410 415
 Val Phe Ile Ile Trp Thr Thr Met Lys Phe Arg Ile Val Thr Cys Gln
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 Ser Val Ser Tyr Lys His Ile Tyr Glu
 435 440

<210> 35

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 35

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 aacactactt ttctgatatg agggcagcac ctgcctctga atgggaaatc atgcaactac 1440

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atctggttac ctgtgcagtt gtgaataccc agagggttggg cagatcagtg tctctagtcc 1560
taccagttt taaagttcat ggtaagattt gacctcatct cccgcaaata aatgtattgg 1620
tgatttgtaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1670

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<210> 36

<211> 164

<212> PRT

<213> Homo sapiens

<400> 36

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Met Gly Gly Met Val Arg Glu Glu Ala Leu Ala Trp Met Cys Arg Glu
  1                      5                      10                      15

Pro Arg Lys Ala Phe Ser Ala Ile Val Gly Pro Ser Leu Gly Pro Asp
          20                      25                      30

Ser Thr Pro Gly Trp Gly Thr Gly Glu Trp Ala Thr Gly Gly Ala Ile
          35                      40                      45

Leu Gly Arg Pro Thr Pro Cys Ala Val Pro Gly Thr Gly Phe Ser Leu
  50                      55                      60

Leu Ser Thr Cys Ser Ser Pro Arg Gly Pro Val Pro Glu Thr Gly Arg
  65                      70                      75                      80

Gly Trp Arg Val Pro Thr Pro Cys Ser Leu Pro Asp Leu Leu Arg Asp
          85                      90                      95

Asp Asp Ala Val Cys Val Pro His Val Gly Pro Pro Pro Ala Cys His
          100                     105                     110

Leu Asn Ala Leu His Gly Pro Val Cys Gly Thr Gly Gly Gln Val Gln
          115                     120                     125

Trp Cys Ala Glu Leu His Trp Glu Asp Phe Gln Arg Gly Arg Ala Ala
          130                     135                     140

Gly Ile Leu Arg Trp Ile Asn Pro Ser Pro Pro Gly Arg Cys Gly Phe
          145                     150                     155                     160

Leu Val Gly Leu

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<210> 37

<211> 1493

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1415)

<400> 37

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catgatcctg gccagcctgc tcatcgccct ctgcagtcag ctggccgcgc gcacctgtga 240
gattgtgacc ttggaccggg acagcagcca gcctcggagg acgatcgccc ggcagaccgc 300

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<210> 38

<211> 132

<212> PRT

<213> Homo sapiens

<400> 38

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Met Ala Pro Ser Pro Arg Thr Gly Ser Arg Gln Asp Ala Thr Ala Leu
  1              5              10              15

Pro Ser Met Ser Ser Thr Phe Trp Ala Phe Met Ile Leu Ala Ser Leu
      20              25              30

Leu Ile Ala Tyr Cys Ser Gln Leu Ala Ala Gly Thr Cys Glu Ile Val
      35              40              45

Thr Leu Asp Arg Asp Ser Ser Gln Pro Arg Arg Thr Ile Ala Arg Gln
      50              55              60

Thr Ala Arg Cys Ala Cys Arg Lys Gly Gln Ile Ala Gly Thr Thr Arg
      65              70              75              80

Ala Arg Pro Ala Cys Val Asp Ala Arg Ile Ile Lys Thr Lys Gln Trp
      85              90              95

Cys Asp Met Leu Pro Cys Leu Glu Gly Glu Gly Cys Asp Leu Leu Ile
      100              105              110

Asn Arg Ser Gly Trp Thr Cys Thr Gln Pro Gly Gly Arg Ile Lys Thr
      115              120              125

Thr Thr Val Ser
      130

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<210> 39

<211> 3693

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (108)

<400> 39

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<210> 40

<211> 230

<212> PRT

<213> Homo sapiens

<400> 40

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Met Leu Arg Phe Val Gln Lys Arg Gly Asn Ser Thr Val Tyr Glu Trp
 1             5             10             15

Arg Thr Gly Thr Glu Pro Ser Val Val Glu Arg Pro His Leu Glu Glu
      20             25             30

Leu Pro Glu Gln Val Ala Glu Asp Ala Ile Asp Trp Gly Asp Phe Gly
      35             40             45

Val Glu Ala Val Ser Glu Gly Thr Asp Ser Gly Ile Ser Ala Glu Ala
      50             55             60

Ala Gly Ile Asp Trp Gly Ile Phe Pro Glu Ser Asp Ser Lys Asp Pro
      65             70             75             80

Gly Gly Asp Gly Ile Asp Trp Gly Asp Asp Ala Val Ala Leu Gln Ile
      85             90             95

Thr Val Leu Glu Ala Gly Thr Gln Ala Pro Glu Gly Val Ala Arg Gly
      100            105            110

Pro Asp Ala Leu Thr Leu Leu Glu Tyr Thr Glu Thr Arg Asn Gln Phe
      115            120            125

Leu Asp Glu Leu Met Glu Leu Glu Ile Phe Leu Ala Gln Arg Ala Val
      130            135            140

Glu Leu Ser Glu Glu Ala Asp Val Leu Ser Val Ser Gln Phe Gln Leu
      145            150            155            160

Ala Pro Ala Ile Leu Gln Gly Gln Thr Lys Glu Lys Met Val Thr Met
      165            170            175

Val Ser Val Leu Glu Asp Leu Ile Gly Lys Leu Thr Ser Leu Gln Leu
      180            185            190

Gln His Leu Phe Met Ile Leu Ala Ser Pro Arg Ser Gly Phe Pro Leu
      195            200            205

Met Gln Gly Ser Ala Ile Leu Ser Ser Ser Ala Ser Leu Tyr Ser Ser
      210            215            220

Ser Cys Ser Met Thr Pro
      225            230

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<210> 41
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<400> 41
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 aaggcctccc agcatctggg actcgagagt gggcagcccc tctacctcct ggagctgaac 180
 tgggggtggaa ctgagtgtgt tcttagctct accgggagga cagctgcctg tttcctcccc 240
 accagcctcc tccccacatc cccagctgcc tggctgggtc ctgaagccct ctgtctacct 300
 gggagaccag ggaccacagg ccttagggat acagggggtc cccttctgtt accaccccc 360
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 cacggcgatt ctcccatgg gatcttgagg gaccaagctg ctgggattgg gaaggagttt 480
 caccctgacc gttgccctag ccaggttccc aggaggcctc accatactcc ctttcagggc 540
 cagggctcca gcaagcccag ggcaaggatc ctgtgctgct gtctggttga gacctgcca 600
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<210> 42
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Lys Asp Val Gly Pro Glu Ser Cys Gly Gln Pro Thr Pro Cys Trp
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 Pro Ser Pro Ala Leu Glu Ser Val Leu Gly Lys Ala Ser Gln His Leu
 20 25 30
 Gly Leu Glu Ser Gly Gln Pro Leu Tyr Leu Leu Glu Leu Asn Trp Gly
 35 40 45
 Gly Thr Glu Cys Val Leu Ser Thr Gly Arg Thr Ala Ala Cys Phe
 50 55 60
 Leu Pro Thr Ser Leu Leu Pro Thr Ser Pro Ala Ala Trp Leu Gly Pro
 65 70 75 80
 Glu Ala Leu Cys Leu Pro Gly Arg Pro Gly Thr Thr Gly Leu Arg Asp
 85 90 95

Thr Gly Gly Pro Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Thr
 100 105 110
 Thr Arg Trp Cys Trp Met Leu Val Leu Trp Pro Ala Lys Val His Gly
 115 120 125
 Asp Ser Pro His Gly Ile Leu Arg Asp Gln Ala Ala Gly Ile Gly Lys
 130 135 140
 Glu Phe His Pro Asp Arg Cys Pro Ser Gln Val Pro Arg Arg Pro His
 145 150 155 160
 His Thr Pro Phe Gln Gly Gln Gly Ser Ser Lys Pro Arg Ala Arg Ile
 165 170 175
 Leu Cys Cys Cys Leu Val Glu Ser Leu Pro Pro Cys Val Gly Ser Val
 180 185 190
 Gly Gln Ala Glu Cys Ile Gly Asp Arg Ala Val Ser Met Gly Leu Gly
 195 200 205
 Val Cys Glu Leu Arg Pro Arg Cys Ala Val Trp Arg Arg Val Leu Ser
 210 215 220
 Gly Lys Arg Cys Gly Phe Lys Val Cys Val Cys Arg Gly Trp Val Cys
 225 230 235 240

<210> 43

<211> 1784

<212> DNA

<213> Homo sapiens

<400> 43

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 cttgctgaat taaatattta tgagtgggtc atttttaagt atagtgaaca agacaccata 180
 ttaagtacag tgataaagca tctatattct gtaaaaaaaaa aaaaaatctg cctatgcatg 240
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 tctgacatat actggaaatg tatgtatact ggcgtacttt atattctcta aaatgcttaa 360
 tgcctttgaa attttgtaat caaaaaaaaa ctttgaaaaa tctaaagggg agagtattct 420
 ttaaagtttt taacataaagc ttgtcaatgc acatgtagat ggtagcatg ttagcaaac 480
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<210> 44
 <211> 82
 <212> PRT
 <213> Homo sapiens

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<400> 44
Met Cys His Lys Ile Cys Thr Phe Phe Thr Phe Phe Pro Leu Tyr Ile
  1             5             10             15
Ser Tyr Gly Leu Gln Leu Val His Ser Glu Asn Asn Asn Asn Lys Ser
          20             25             30
Pro Phe Ile Phe Phe Asn Asn Cys Ile Ser Ala Gln Val Ile His Tyr
          35             40             45
Ser Leu Lys Pro Cys Leu Cys Asn Leu Thr Ser Asp Met Leu Ala Ile
          50             55             60
Lys Ala Cys Thr Cys Asn Asn Glu Lys Glu Lys Ala Phe Tyr Ile Thr
          65             70             75             80
Thr Gln

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<210> 45
 <211> 1034
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (598)

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<400> 45
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aaaaaaaaaa aaaa 1034

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<210> 46

<211> 126
 <212> PRT
 <213> Homo sapiens

<400> 46

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Met Ala Ala Ser Gly Ala Glu Pro Gln Val Leu Val Gln Tyr Leu Val
  1              5              10              15

Leu Arg Lys Asp Leu Ser Gln Ala Pro Phe Ser Trp Pro Ala Gly Ala
      20              25              30

Leu Val Ala Gln Ala Cys His Ala Ala Thr Ala Ala Leu His Thr His
      35              40              45

Arg Asp His Pro His Thr Ala Ala Tyr Leu Gln Glu Leu Gly Arg Met
      50              55              60

Arg Lys Val Val Leu Glu Ala Pro Asp Glu Thr Thr Leu Lys Glu Leu
      65              70              75              80

Ala Glu Thr Leu Gln Gln Lys Asn Ile Asp His Met Leu Trp Leu Glu
      85              90              95

Gln Pro Glu Asn Ile Ala Thr Cys Ile Ala Leu Arg Pro Tyr Pro Lys
      100             105             110

Glu Glu Val Gly Gln Tyr Leu Lys Lys Phe Arg Leu Phe Lys
      115             120             125

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<210> 47
 <211> 1626
 <212> DNA
 <213> Homo sapiens

<400> 47

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aaagagaaac ctcaatgagt tatggaattt cctttttggt gaattgagtg ctgtttttgc 240
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tctactaaaa attcagaaaa ttagctgggc atgggtggcac gtgcctgtag tcccagctac 1440

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tcaggaggct gaggaagag aattgcttga acccaggagg tggagggttgc agtgagctga 1500
 gattgcaccg ctgccctcca gcctgggtga cagagcaaga ctccatttca aataaataaa 1560
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 aaaaaa 1626

<210> 48

<211> 368

<212> PRT

<213> Homo sapiens

<400> 48

Met Ile Leu Pro Lys Arg Asn Leu Asn Glu Leu Trp Asn Phe Leu Phe
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 Gly Glu Leu Ser Ala Val Phe Ala Phe Leu Arg Phe Gln Met Arg Val
 20 25 30
 Tyr Ile Phe Leu Cys Leu Met Cys Trp Val Arg Ser Asp Asn Lys Arg
 35 40 45
 Pro Cys Leu Glu Phe Ser Gln Leu Ser Val Lys Asp Ser Phe Arg Asp
 50 55 60
 Leu Phe Ile Pro Arg Ile Glu Thr Ile Leu Met Met Tyr Thr Arg Asn
 65 70 75 80
 Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu Asn
 85 90 95
 Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly Tyr
 100 105 110
 Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg Ile
 115 120 125
 Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser Arg
 130 135 140
 Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg Lys
 145 150 155 160
 Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His Gly
 165 170 175
 Ala Ser Leu Asp Asn Phe His Phe Ile Gly Val Ser Leu Gly Ala His
 180 185 190
 Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg Ile
 195 200 205
 Thr Gly Leu Asp Pro Ala Gly Pro Arg Phe Ser Arg Lys Pro Pro Tyr
 210 215 220
 Ser Arg Leu Asp Tyr Thr Asp Ala Lys Phe Val Asp Val Ile His Ser
 225 230 235 240
 Asp Ser Asn Gly Ile Gln Phe Ile Lys Cys Asn His Gln Arg Ala Val
 245 250 255
 His Leu Phe Met Ala Ser Leu Glu Thr Asn Cys Asn Phe Ile Ser Phe

260	265	270
Pro Cys Arg Ser Tyr Lys Asp	Tyr Lys Thr Ser Leu Cys Val Asp Cys	
275	280	285
Asp Cys Phe Lys Glu Lys Ser Cys	Pro Arg Leu Gly Tyr Gln Ala Lys	
290	295	300
Leu Phe Lys Gly Val Leu Lys Glu Arg Met	Glu Gly Arg Pro Leu Arg	
305	310	315
Thr Thr Val Phe Leu Asp Thr Ser Ala Tyr Tyr	Phe Val Leu Ser Ile	
325	330	335
Ile Val Pro Asp Lys Thr Met Met Asp Gly Ser	Phe Ser Phe Lys Leu	
340	345	350
Leu Asn Gln Leu Gly Met Ile Glu Glu Pro Arg	Leu Tyr Glu Glu Arg	
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<210> 49

<211> 1221

<212> DNA

<213> Homo sapiens

<400> 49

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tcatgttcca ttcttctgca atggttaatt cacacagaaa accaatgttt aacattcaca 240
gaggatttta ctgcttaaca gccatcttgc cccaaatatg catttgttct cagttctcag 300
tgccatctag ttatcacttc actgaggatc ctggggcttt ccagtagacc actaatgggg 360
aacgatttcc ttggcaggag ctaaggctcc ccagtgtggt cattcctctc cattatgacc 420
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1221

<210> 50

<211> 305

<212> PRT

<213> Homo sapiens

<400> 50

Met Phe His Ser Ser Ala Met Val Asn Ser His Arg Lys Pro Met Phe
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20 25 30

Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu
 35 40 45
 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp
 50 55 60
 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu
 65 70 75 80
 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys
 85 90 95
 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser
 100 105 110
 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser
 115 120 125
 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala
 130 135 140
 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu
 145 150 155 160
 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe
 165 170 175
 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg
 180 185 190
 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe
 195 200 205
 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile
 210 215 220
 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Ser
 225 230 235 240
 Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln
 245 250 255
 Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr
 260 265 270
 Tyr Pro Leu Ser Lys Leu Gly Met Phe Lys Phe His Ile Ile Val Phe
 275 280 285
 Ile Phe Ala His Lys Thr Cys Leu Asp Leu Phe Pro Leu Ser Leu Cys
 290 295 300
 Met
 305

<210> 51

<211> 951

<212> DNA

<213> Homo sapiens

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<400> 51
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cggtcacctc cccccagcac cacctccagc cctgcgcct cggaggcaga cagtggggag 240
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gatgtactat tgggtggaaga atgaactgga gcagcctttc tggagagtga tttgccaata 780
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gtttgtaaac atggatgtgt gcaaagattt tagctctaag aatgtttgtc agtggttctaa 900
taatagcaaa aaataaaaaa caaatgattg aaaaataaaa aaaaaaaaaa a 951

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<210> 52

<211> 194

<212> PRT

<213> Homo sapiens

<400> 52

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          20                      25                      30

Gln Pro Arg Ser Ile Ser Glu Ser Phe Leu Thr Val Lys Gly Ala Ala
          35                      40                      45

Leu Phe Leu Pro Arg Gly Asn Gly Ser Ser Thr Pro Arg Ile Ser His
          50                      55                      60

Arg Arg Asn Lys His Ala Gly Asp Leu Gln Gln His Leu Gln Ala Met
          65                      70                      75                      80

Phe Ile Leu Leu Arg Pro Glu Asp Asn Ile Arg Leu Ala Val Arg Leu
          85                      90                      95

Glu Ser Thr Tyr Gln Asn Arg Thr Arg Tyr Met Val Val Val Ser Thr
          100                      105                      110

Asn Gly Arg Gln Asp Thr Glu Glu Ser Ile Val Leu Gly Met Asp Phe
          115                      120                      125

Ser Ser Asn Asp Ser Thr Cys Thr Met Gly Leu Val Leu Pro Leu Trp
          130                      135                      140

Ser Asp Thr Leu Ile His Leu Asp Gly Asp Gly Gly Phe Ser Val Ser
          145                      150                      155                      160

Thr Asp Asn Arg Val His Ile Phe Lys Pro Val Ser Val Gln Ala Met
          165                      170                      175

Trp Val Asp Arg Asp Ser Arg Asn Lys His Cys Asp Val Leu Leu Val
          180                      185                      190

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Glu Glu

<210> 53
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 53
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 caagtctttg agtggacata tatttgcgtt tctcttgagt gaatgcacct tgttgggtca 240
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 tatctcataa ttttattttc ttgtttaatg atgttgagtg tatttcattt gtattttagt 360
 ttgcaaagt ttgttcaa tcttcacctg ttttaaatga agacgtacga cttatttttg 420
 tgttctgaac ataagttctt tgtcacataa aatgtgctat gaatggtgag ttttaaatac 480
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 aacaattttac tttattgctc taaaatagaa aagttgccag aatgctgtgg agtttttagtg 600
 gaaaacatga tagctggtgt tactgagtaa atttgagtgt taaatgtcaa tgtaagctaa 660
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 tagcacagag cgtgtcatat aatatggctt cacaagtacc ctcattctct tccagtcgt 960
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 aatcacctag gtgtgggccc ggcacggtgg ctaacgcctg tgggtcccagc actttgggat 1260
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 aaaaaaaaaa aaaa 1514

<210> 54
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 54
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 20 25 30
 Pro Leu His Phe Tyr Phe Phe Ile Gln Gln Val Leu Ile Lys Cys Ala
 35 40 45
 Leu Tyr Gln Val Leu Ser Ser Ser Leu Gly Tyr Asn Gly Asp Gln Gly
 50 55 60
 Asp Cys Arg Phe Trp Gln Gly Lys Leu Thr Ser Asn Thr Ala Thr Arg
 65 70 75 80
 His Ser Glu Thr Leu Ser Leu Leu Glu Glu Leu

85

90

<210> 55
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<400> 55
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 agcagtcaac caacataatct ctttcccaga gtcccatgaa taatcttcag actaacacag 180
 tagcccaaga agcatttttt gcagcaccga actcaatttc tccacttcag tcaacatcaa 240
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 tgctttccca agaacaggca caacccccgc agcagggttt atttcagcct cagggtggccc 360
 tgggctccct tccacctaata ccaatgcctc aaagccaaca aggaaccatg ttccagtcac 420
 agcactcaat agttgccatg cagagtaact ctccatccca ggaacagcag cagcagcagc 480
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 ccatggctac aatggcgtct ccaaagcaac caccaccaa catgatattc aacccaaatc 600
 aaaatccaat ggctaatacag gagcaacaga accagtcaat ttttcaccaa caaagtaaca 660
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<210> 56
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 56
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 20 25 30
 Gln Ser Pro Met Asn Asn Leu Gln Thr Asn Thr Val Ala Gln Glu Ala
 35 40 45
 Phe Phe Ala Ala Pro Asn Ser Ile Ser Pro Leu Gln Ser Thr Ser Asn
 50 55 60
 Ser Glu Gln Gln Ala Ala Phe Gln Gln Gln Ala Pro Ile Ser His Ile
 65 70 75 80
 Gln Thr Pro Met Leu Ser Gln Glu Gln Ala Gln Pro Pro Gln Gln Gly
 85 90 95
 Leu Phe Gln Pro Gln Val Ala Leu Gly Ser Leu Pro Pro Asn Pro Met
 100 105 110

Pro Gln Ser Gln Gln Gly Thr Met Phe Gln Ser Gln His Ser Ile Val
 115 120 125
 Ala Met Gln Ser Asn Ser Pro Ser Gln Glu Gln Gln Gln Gln Gln
 130 135 140
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Ile Leu Phe Ser
 145 150 155 160
 Asn Gln Asn Thr Met Ala Thr Met Ala Ser Pro Lys Gln Pro Pro Pro
 165 170 175
 Asn Met Ile Phe Asn Pro Asn Gln Asn Pro Met Ala Asn Gln Glu Gln
 180 185 190
 Gln Asn Gln Ser Ile Phe His Gln Gln Ser Asn Met Ala Pro Met Asn
 195 200 205
 Gln Glu Gln Gln Pro Met Gln Phe Gln Ser Gln Ser Thr Val Ser Ser
 210 215 220
 Leu Gln Asn Pro Gly Pro Thr Gln Ser Glu Ser Ser Gln Thr Pro Leu
 225 230 235 240
 Phe His Ser Ser Pro Gln Ile Gln Leu Val Gln Gly Ser Pro Ser Ser
 245 250 255
 Gln Glu Gln Gln Val Thr Leu Phe Leu Ser Pro Ala Ser Met Ser Ala
 260 265 270
 Leu Gln Thr Ser Ile Asn Gln Gln Asp Met Gln Gln Ser Pro Leu Tyr
 275 280 285
 Ser Pro Gln Asn Asn Met Pro Gly Ile Gln Gly Ala Thr Phe Ser Pro
 290 295 300
 Gln Pro Gln Ala Thr Leu Phe His Asn Thr Ala Gly Gly Thr Met Asn
 305 310 315 320
 Gln Leu Gln Asn Ser Pro Gly Ser Ser Gln Gln Thr Ser Gly Met Phe
 325 330 335
 Leu Phe Gly Ile Gln Asn Asn Cys Ser Gln Leu Leu Thr Ser Gly Pro
 340 345 350
 Ala Thr Leu Pro Asp Gln Leu Met Ala Ile Ser Gln Pro Gly Gln Pro
 355 360 365
 Gln Asn Glu Gly Gln Pro Pro Val Thr Thr Leu Leu Ser Gln Gln Met
 370 375 380
 Pro Glu Asn Ser Pro Leu Ala Ser Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Glu Lys Ile Asp Leu Leu Val Ser Leu Gln Asn Gln Gly Asn Asn Leu
 405 410 415
 Thr Gly Ser Phe
 420

<210> 57
 <211> 2297
 <212> DNA
 <213> Homo sapiens

<400> 57
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 ttcgtggcta ctttggggaa acaattgctc tgtactttgg atttttggag tatttcactt 180
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 gtaaaaaaaaa aaaaaaa 2297

<210> 58
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 58
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 20 25 30

Ile Leu Glu Leu Trp Lys Arg Gly Cys Ala Asn Met Thr Tyr Arg Trp
 35 40 45
 Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu Pro Arg Pro Gly Phe
 50 55 60
 His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly Lys Glu Glu Pro Leu
 65 70 75 80
 Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr Leu Val Ser Leu Pro
 85 90 95
 Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr Val Met Met Ile Tyr
 100 105 110
 Phe Asp Met Glu Val Trp Ala Leu Gly Leu His Glu Asn Ser Gly Ser
 115 120 125
 Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser Ile Ile Tyr Ala Ile
 130 135 140
 Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr Ala Ala Glu Phe Leu
 145 150 155 160
 Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala Tyr Gln Asn His Leu
 165 170 175
 Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn Cys Phe Ala Ser Leu
 180 185 190
 Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys Leu Leu Arg Gln Ser
 195 200 205
 Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu Asn Gln Ile Met Glu
 210 215 220
 Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His Gly Val Gln Val Lys
 225 230 235 240
 Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp Ala Thr Leu Tyr Glu
 245 250 255
 Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr Leu Gly Thr Phe Asp
 260 265 270
 Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr Val Ser Leu Phe Ser
 275 280 285
 Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val Leu Asn Asn Phe Thr
 290 295 300
 Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg Val Phe Lys Arg Pro
 305 310 315 320
 Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp Gln Met Ile Phe Cys
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Leu Leu Gly Glu Met Glu Met Ser Cys Val Leu Phe Val Val Val Val
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Val Ser Gln Val Asn Thr Pro Ile Lys Arg
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<210> 59

<211> 4145

<212> DNA

<213> Homo sapiens

<400> 59

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<211> 289

<212> PRT

<213> Homo sapiens

<400> 60

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      20             25             30

Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys
  35             40             45

Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn
  50             55             60

Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala
  65             70             75             80

Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys
      85             90             95

Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys
  100            105            110

Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys
  115            120            125

Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro
  130            135            140

Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala Pro Thr Pro
  145            150            155            160

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Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro Gln Pro Pro
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Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala Pro Ser Ala
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Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro Ala Pro Ser
 195 200 205

Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr
 210 215 220

Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met
 225 230 235 240

Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro
 245 250 255

Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln
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Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln
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 <212> DNA
 <213> Homo sapiens

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<210> 62

<211> 414
 <212> PRT
 <213> Homo sapiens

<400> 62

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Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu
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 35 40 45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
 50 55 60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
 65 70 75 80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
 85 90 95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
 100 105 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
 115 120 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
 130 135 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
 145 150 155 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
 165 170 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
 180 185 190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
 195 200 205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
 210 215 220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
 225 230 235 240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
 245 250 255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
 260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
 275 280 285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn

290 295 300
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
 305 310 315 320
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 325 330 335
 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val
 340 345 350
 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly
 355 360 365
 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys
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 <211> 1571
 <212> DNA
 <213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 64

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          20              25              30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
          35              40              45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
 50              55              60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
 65              70              75              80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
          85              90              95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
          100              105              110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
 115              120              125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
 130              135              140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys
 145              150              155              160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu
          165              170              175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu
          180              185              190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu
          195              200              205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu
 210              215              220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro
 225              230              235              240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu
          245              250              255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu
          260              265              270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu
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Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val
 290              295              300

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Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu
 305 310 315 320

Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr Lys Lys Ala Leu
 325 330 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys
 340 345 350

Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Gln Asp Ile Leu
 355 360 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln Thr Gly Arg Ile
 370 375 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp
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<210> 65

<211> 1752

<212> DNA

<213> Homo sapiens

<400> 65

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 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 66
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 35 40 45
 Thr Thr Ala Thr His Cys Gly Val Pro Asn Tyr Leu Pro Ser Val Ser
 50 55 60
 Ser Ala Ile Gly Gly Glu Val Pro Gln Arg Tyr Val Trp Arg Phe Cys
 65 70 75 80
 Ile Gly Leu His Ser Ala Pro Arg Phe Leu Val Ala Phe Ala Tyr Trp
 85 90 95
 Asn His Tyr Leu Ser Cys Thr Ser Pro Cys Ser Cys Tyr Arg Pro Leu
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 Cys Arg Leu Asn Phe Gly Leu Asn Val Val Glu Asn Leu Ala Leu Leu
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 Val Leu Thr Tyr Val Ser Ser Ser Glu Asp Phe Thr Ile His Glu Asn
 130 135 140
 Ala Phe Ile Val Phe Ile Ala Ser Ser Leu Gly His Met Leu Leu Thr
 145 150 155 160
 Cys Ile Leu Trp Arg Leu Thr Lys Lys His Thr Val Ser Gln Glu Asp
 165 170 175
 Arg Lys Ser Tyr Ser Trp Lys Gln Arg Leu Phe Ile Ile Asn Phe Ile
 180 185 190
 Ser Phe Phe Ser Ala Leu Ala Val Tyr Phe Arg His Asn Met Tyr Cys
 195 200 205
 Glu Ala Gly Val Tyr Thr Ile Phe Ala Ile Leu Glu Tyr Thr Val Val
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<210> 67
 <211> 781

<212> DNA

<213> Homo sapiens

<400> 67

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aaaatatatt ttattcagtt ggctttctgt ggttgtgctc tcaaataatag tgtatgctta 660
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781

<210> 68

<211> 127

<212> PRT

<213> Homo sapiens

<400> 68

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Met Ile Trp Asn Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp
  1             5             10             15

Gly Ile Lys Gln Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu
          20             25             30

Met Gly Leu Leu Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg
  35             40             45

Thr Met Met Phe Ser Leu Asp Thr Thr Thr Trp Glu Tyr Pro Asp Val
  50             55             60

Cys Arg His Tyr Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe
  65             70             75             80

Ser Leu Val Ser Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met
          85             90             95

Ser Asn Phe Leu Phe Asn Thr Gly Lys Phe Ile Phe Ser Lys Tyr Leu
 100             105             110

Tyr His Met Leu Leu Thr Gln Tyr Phe Gln Ile Leu Leu Pro Leu
 115             120             125

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<210> 69

<211> 649

<212> DNA

<213> Homo sapiens

<400> 69

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gaacccccagg ggaaggtgca atacggagag cactttcgga ttcggcagaa tctaccagag 180
cacacccaag gctggccttg gagcaaattg ctctggcttc tttttgttgt tgtgccgttt 240

```

```

gtgatactgc agtgtcaaag agacagtgcg aagaataagg agcagagtcc tccctggcctt 300
cgaggcggcc aacttcactc tccattaaag aaaaaaagaa atgcttcccc caacaaagac 360
tgtgcattca ataccttaat ggaactcgag gtggagctta tgaaatttgt gtccaaagtg 420
cggaatctta aacgtgccat ggcaacaggt agtggcagta acctcaggct tcgaaagtca 480
gagatgcctg cagatccata ccatgtcacg atctgtgaaa tatggggaga agaaagctct 540
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actaataaaa ctattctgaa gaaaagaaaa aaaaaaaaaa aaaaaaaaaa 649

```

<210> 70

<211> 171

<212> PRT

<213> Homo sapiens

<400> 70

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Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys
  1                      5                      10                      15
Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro
          20                      25                      30
Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu
          35                      40                      45
Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu
          50                      55                      60
Phe Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu
          65                      70                      75                      80
Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His
          85                      90                      95
Ser Pro Leu Lys Lys Lys Arg Asn Ala Ser Pro Asn Lys Asp Cys Ala
          100                     105                     110
Phe Asn Thr Leu Met Glu Leu Glu Val Glu Leu Met Lys Phe Val Ser
          115                     120                     125
Lys Val Arg Asn Leu Lys Arg Ala Met Ala Thr Gly Ser Gly Ser Asn
          130                     135                     140
Leu Arg Leu Arg Lys Ser Glu Met Pro Ala Asp Pro Tyr His Val Thr
          145                     150                     155                     160
Ile Cys Glu Ile Trp Gly Glu Glu Ser Ser Ser
          165                     170

```

<210> 71

<211> 1456

<212> DNA

<213> Homo sapiens

<400> 71

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gtgcctgcct gtggcaacce caccattcac cctggacagt gctgcccata atgtgcagat 240
gactttgtgg tgcagaagcc agagctcagt actccctcca ttgcccacgc ccctggagga 300
gaatactttg tggaaggaga aacgtggaac attgactcct gtactcagtg cacctgccac 360

```

```

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cgcaataaca gcgtacctaa ttattgcaaa aatgatgaag gggatatatt cctggcagct 540
gagtcctgga agcctgacgt ttgtaccagc tgcatctgca ttgatacgct aattagctgt 600
ttctctgagt cctgcccttc tgtatcctgt gaaagacctg tcttgagaaa aggccagtgt 660
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cctagtga aa atgatatcgt ccatctccct agagatatgg gtcacctcca ggtagattac 1020
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aaaaaaaaa aaaaaa 1456

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<210> 72

<211> 400

<212> PRT

<213> Homo sapiens

<400> 72

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Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr
  1                      5                      10                      15

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Ile His Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val
                20                      25                      30

```

```

Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly
  35                      40                      45

```

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Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln
  50                      55                      60

```

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Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro
  65                      70                      75                      80

```

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Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro
                85                      90                      95

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Gln Cys Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser
  100                      105                      110

```

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Val Pro Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala
  115                      120                      125

```

```

Glu Ser Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser
  130                      135                      140

```

```

Val Ile Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg
  145                      150                      155                      160

```

```

Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr
                165                      170                      175

```

```

Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp

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<210> 73
<211> 4723
<212> DNA
<213> Homo sapiens
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65

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<210> 74

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 74

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Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
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Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
      20              25              30

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35              40              45

Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50              55              60

Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65              70              75              80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85              90              95

Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
      100             105             110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
      115             120             125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
      130             135             140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
      145             150             155             160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
      165             170             175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
      180             185             190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
      195             200             205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
      210             215             220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
      225             230             235             240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg

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245										250					255				
Thr	Val	Glu	Cys	Pro	Pro	Val	Gln	Gln	Thr	Ala	Cys	Pro	Pro	Asp	Ser				
			260						265					270					
Tyr	Glu	Thr	Gln	Val	Arg	Leu	Thr	Ala	Asp	Gly	Cys	Cys	Thr	Leu	Pro				
		275					280						285						
Thr	Arg	Cys	Glu	Cys	Leu	Ser	Gly	Leu	Cys	Gly	Phe	Pro	Val	Cys	Glu				
		290				295					300								
Val	Gly	Ser	Thr	Pro	Arg	Ile	Val	Ser	Arg	Gly	Asp	Gly	Thr	Pro	Gly				
305					310					315					320				
Lys	Cys	Cys	Asp	Val	Phe	Glu	Cys	Val	Asn	Asp	Thr	Lys	Pro	Ala	Cys				
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Val	Phe	Asn	Asn	Val	Glu	Tyr	Tyr	Asp	Gly	Asp	Met	Phe	Arg	Met	Asp				
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Asn	Cys	Arg	Phe	Cys	Arg	Cys	Gln	Gly	Gly	Val	Ala	Ile	Cys	Phe	Thr				
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Glu	Cys	Cys	Pro	Val	Cys	Glu	Asp	Pro	Val	Tyr	Pro	Phe	Asn	Asn	Pro				
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Ala	Gly	Cys	Tyr	Ala	Asn	Gly	Leu	Ile	Leu	Ala	His	Gly	Asp	Arg	Trp				
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Arg	Glu	Asp	Asp	Cys	Thr	Phe	Cys	Gln	Cys	Val	Asn	Gly	Glu	Arg	His				
			420					425					430						
Cys	Val	Ala	Thr	Val	Cys	Gly	Gln	Thr	Cys	Thr	Asn	Pro	Val	Lys	Val				
		435					440					445							
Pro	Gly	Glu	Cys	Cys	Pro	Val	Cys	Glu	Glu	Pro	Thr	Ile	Ile	Thr	Val				
		450				455					460								
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465					470					475					480				
Asp	Cys	Ile	Asn	Gly	Phe	Lys	Arg	Asp	His	Asn	Gly	Cys	Arg	Thr	Cys				
				485					490					495					
Gln	Cys	Ile	Asn	Thr	Glu	Glu	Leu	Cys	Ser	Glu	Arg	Lys	Gln	Gly	Cys				
			500					505					510						
Thr	Leu	Asn	Cys	Pro	Phe	Gly	Phe	Leu	Thr	Asp	Ala	Gln	Asn	Cys	Glu				
		515					520					525							
Ile	Cys	Glu	Cys	Arg	Pro	Arg	Pro	Lys	Lys	Cys	Arg	Pro	Ile	Ile	Cys				
		530				535					540								
Asp	Lys	Tyr	Cys	Pro	Leu	Gly	Leu	Leu	Lys	Asn	Lys	His	Gly	Cys	Asp				
545					550					555					560				
Ile	Cys	Arg	Cys	Lys	Lys	Cys	Pro	Glu	Leu	Ser	Cys	Ser	Lys	Ile	Cys				

565	570	575
Pro Leu Gly Phe Gln Gln Asp Ser His Gly Cys Leu Ile Cys Lys Cys		
580	585	590
Arg Glu Ala Ser Ala Ser Ala Gly Pro Pro Ile Leu Ser Gly Thr Cys		
595	600	605
Leu Thr Val Asp Gly His His His Lys Asn Glu Glu Ser Trp His Asp		
610	615	620
Gly Cys Arg Glu Cys Tyr Cys Leu Asn Gly Arg Glu Met Cys Ala Leu		
625	630	635
Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr Ile His Pro Gly		
645	650	655
Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val Gln Lys Pro Glu		
660	665	670
Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly Glu Tyr Phe Val		
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Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln Cys Thr Cys His		
690	695	700
Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro Pro Leu Leu Cys		
705	710	715
Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro Gln Cys Thr Asp		
725	730	735
Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser Val Pro Asn Tyr		
740	745	750
Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala Glu Ser Trp Lys		
755	760	765
Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser Val Ile Ser Cys		
770	775	780
Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg Pro Val Leu Arg		
785	790	795
Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr Ile Pro Lys Lys		
805	810	815
Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp		
820	825	830
Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln Gly Gln Thr Leu		
835	840	845
Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn		
850	855	860
Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met Tyr Val Pro Glu		
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Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg Gly Glu Val Asp		
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	885		890		895
Leu Glu Val	Pro Leu Trp Pro Thr	Pro Ser Glu Asn Asp	Ile Val His		
	900	905	910		
Leu Pro Arg Asp Met Gly His	Leu Gln Val Asp Tyr Arg Asp Asn Arg				
	915	920	925		
Leu His Pro Ser Glu Asp Ser Ser	Leu Asp Ser Ile Ala Ser Val Val				
	930	935	940		
Val Pro Ile Ile Ile Cys Leu Ser	Ile Ile Ile Ala Phe Leu Phe Ile				
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Asn Gln Lys Lys Gln Trp Ile Pro	Leu Leu Cys Trp Tyr Arg Thr Pro				
	965	970	975		
Thr Lys Pro Ser Ser Leu Asn Asn	Gln Leu Val Ser Val Asp Cys Lys				
	980	985	990		
Lys Gly Thr Arg Val Gln Val Asp	Ser Ser Gln Arg Met Leu Arg Ile				
	995	1000	1005		
Ala Glu Pro Asp Ala Arg Phe Ser	Gly Phe Tyr Ser Met Gln Lys Gln				
	1010	1015	1020		
Asn His Leu Gln Ala Asp Asn Phe	Tyr Gln Thr Val				
	1025	1030	1035		

<210> 75

<211> 3861

<212> DNA

<213> Homo sapiens

<400> 75

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<210> 76

<211> 457

<212> PRT

<213> Homo sapiens

<400> 76

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Met Arg Lys Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
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Leu Phe Phe Leu Leu Leu Glu Gly Gly Lys Thr Glu Gln Val Lys His
      20             25             30

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
  35             40             45

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
  50             55             60

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Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys
 65 70 75 80
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys
 85 90 95
 Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser
 100 105 110
 Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe
 115 120 125
 Val Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln
 130 135 140
 Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro
 145 150 155 160
 Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg
 165 170 175
 Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp
 180 185 190
 Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg
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 Ser His Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg
 210 215 220
 Phe Pro Gly Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln
 225 230 235 240
 Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His
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 Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser
 260 265 270
 Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys
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 Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn
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 Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys
 305 310 315 320
 Val Cys Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe
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 Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu
 340 345 350
 Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu
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 Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys
 370 375 380

Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe
 385 390 395 400

Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln
 405 410 415

Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser
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Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr
 435 440 445

Leu Glu Arg Ser Glu Lys Gly His Cys
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<210> 77

<211> 2050

<212> DNA

<213> Homo sapiens

<400> 77

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<210> 78

<211> 505

<212> PRT

<213> Homo sapiens

<400> 78

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Met Ser Arg Ser Tyr Asn Asp Glu Leu Gln Phe Leu Glu Lys Ile Asn
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Lys Asn Cys Trp Arg Ile Lys Lys Gly Phe Val Pro Asn Met Gln Val
      20              25              30

Glu Gly Val Phe Tyr Val Asn Asp Ala Leu Glu Lys Leu Met Phe Glu
      35              40              45

Glu Leu Arg Asn Ala Cys Arg Gly Gly Gly Val Gly Gly Phe Leu Pro
 50              55              60

Ala Met Lys Gln Ile Gly Asn Val Ala Ala Leu Pro Gly Ile Val His
 65              70              75              80

Arg Ser Ile Gly Leu Pro Asp Val His Ser Gly Tyr Gly Phe Ala Ile
      85              90              95

Gly Asn Met Ala Ala Phe Asp Met Asn Asp Pro Glu Ala Val Val Ser
      100              105              110

Pro Gly Gly Val Gly Phe Asp Ile Asn Cys Gly Val Arg Leu Leu Arg
      115              120              125

Thr Asn Leu Asp Glu Ser Asp Val Gln Pro Val Lys Glu Gln Leu Ala
      130              135              140

Gln Ala Met Phe Asp His Ile Pro Val Gly Val Gly Ser Lys Gly Val
      145              150              155              160

Ile Pro Met Asn Ala Lys Asp Leu Glu Glu Ala Leu Glu Met Gly Val
      165              170              175

Asp Trp Ser Leu Arg Glu Gly Tyr Ala Trp Ala Glu Asp Lys Glu His
      180              185              190

Cys Glu Glu Tyr Gly Arg Met Leu Gln Ala Asp Pro Asn Lys Val Ser
      195              200              205

Ala Arg Ala Lys Lys Arg Gly Leu Pro Gln Leu Gly Thr Leu Gly Ala
      210              215              220

Gly Asn His Tyr Ala Glu Ile Gln Val Val Asp Glu Ile Phe Asn Glu
      225              230              235              240

Tyr Ala Ala Lys Lys Met Gly Ile Asp His Lys Gly Gln Val Cys Val
      245              250              255

Met Ile His Ser Gly Ser Arg Gly Leu Gly His Gln Val Ala Thr Asp
      260              265              270

Ala Leu Val Ala Met Glu Lys Ala Met Lys Arg Asp Lys Ile Ile Val
      275              280              285

Asn Asp Arg Gln Leu Ala Cys Ala Arg Ile Ala Ser Pro Glu Gly Gln
      290              295              300

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Asp Tyr Leu Lys Gly Met Ala Ala Ala Gly Asn Tyr Ala Trp Val Asn
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 Arg Ser Ser Met Thr Phe Leu Thr Arg Gln Ala Phe Ala Lys Val Phe
 325 330 335
 Asn Thr Thr Pro Asp Asp Leu Asp Leu His Val Ile Tyr Asp Val Ser
 340 345 350
 His Asn Ile Ala Lys Val Glu Gln His Val Val Asp Gly Lys Glu Arg
 355 360 365
 Thr Leu Leu Val His Arg Lys Gly Ser Thr Arg Ala Phe Pro Pro His
 370 375 380
 His Pro Leu Ile Ala Val Asp Tyr Gln Leu Thr Gly Gln Pro Val Leu
 385 390 395 400
 Ile Gly Gly Thr Met Gly Thr Cys Ser Tyr Val Leu Thr Gly Thr Glu
 405 410 415
 Gln Gly Met Thr Glu Thr Phe Gly Thr Thr Cys His Gly Ala Gly Arg
 420 425 430
 Ala Leu Ser Arg Ala Lys Ser Arg Arg Asn Leu Asp Phe Gln Asp Val
 435 440 445
 Leu Asp Lys Leu Ala Asp Met Gly Ile Ala Ile Arg Val Ala Ser Pro
 450 455 460
 Lys Leu Val Met Glu Glu Ala Pro Glu Ser Tyr Lys Asn Val Thr Asp
 465 470 475 480
 Val Val Asn Thr Cys His Asp Ala Gly Ile Ser Lys Lys Ala Ile Lys
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 Leu Arg Pro Ile Ala Val Ile Lys Gly
 500 505

<210> 79

<211> 1178

<212> DNA

<213> Homo sapiens

<400> 79

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<210> 80

<211> 310

<212> PRT

<213> Homo sapiens

<400> 80

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Met Ser His Ser Ser Ser Gly Ser Ala Ser Leu Ser Gln Val Ser Pro
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Gly Lys Glu Thr Asp Gln Thr Glu Thr Val Ser Val Gln Ser Ser Val
      20              25              30

Leu Gly Lys Gly Val Lys His Arg Pro Pro Pro Ile Lys Leu Pro Ser
      35              40              45

Ser Ser Gly Asn Ser Ser Ser Gly Asn Tyr Phe Thr Pro Gln Gln Thr
      50              55              60

Ser Ser Phe Leu Lys Ser Pro Thr Pro Pro Pro Ser Ser Lys Pro Ser
      65              70              75              80

Ser Ile Pro Arg Lys Ser Ser Val Asp Leu Asn Gln Val Ser Met Leu
      85              90              95

Ser Pro Ala Ala Leu Ser Pro Ala Ser Ser Ser Gln Arg Thr Thr Ala
      100             105             110

Thr Gln Val Met Ala Asn Ser Ala Gly Leu Asn Phe Ile Asn Val Val
      115             120             125

Gly Ser Val Cys Gly Ala Gln Ala Leu Met Ser Gly Ser Asn Pro Met
      130             135             140

Leu Gly Cys Asn Thr Gly Ala Ile Thr Pro Ala Gly Ile Asn Leu Ser
      145             150             155             160

Gly Leu Leu Pro Ser Gly Gly Leu Leu Pro Asn Ala Leu Pro Ser Ala
      165             170             175

Met Gln Ala Ala Ser Gln Ala Gly Val Pro Phe Gly Leu Lys Asn Thr
      180             185             190

Ser Ser Leu Arg Pro Leu Asn Leu Leu Gln Leu Pro Gly Gly Ser Leu
      195             200             205

Ile Phe Asn Thr Leu Gln Gln Gln Gln Gln Leu Ser Gln Phe Thr
      210             215             220

Pro Gln Gln Pro Gln Gln Pro Thr Thr Cys Ser Pro Gln Gln Pro Gly
      225             230             235             240

Glu Gln Gly Ser Glu Gln Gly Ser Thr Ser Gln Glu Gln Ala Leu Ser

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<210> 83
<211> 832

<212> DNA

<213> Homo sapiens

<400> 83

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tttatgaatt tgatgaagtg atgtttccaa agaacgtgag gtgctctact tgtgatttaa 180
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aacattcact cccatgggct tcggagcaac cttcaagaga tctttctacc tgcctttcca 720
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<210> 84

<211> 144

<212> PRT

<213> Homo sapiens

<400> 84

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Met Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro
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Ala Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe
          20              25              30

Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile
      35              40              45

Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr
      50              55              60

Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser
      65              70              75              80

Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu Pro Cys
          85              90              95

Tyr Gly His Gly Leu Ser Tyr Ser Val Pro Val Pro Asp Phe Ser Thr
      100              105              110

Asp Cys Leu His Ala Gly Leu Cys Arg Gly Ser Glu Leu Pro Pro Gly
      115              120              125

Trp Leu Pro Val Val Cys Pro Val Ser Gly Gly His Gln Pro Asp Tyr
      130              135              140

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<210> 85

<211> 3790

<212> DNA

<213> Homo sapiens

<400> 85

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aacggcagtc tcaatctggc cccacacctt tcttgggctt gtaggaaggt ggacatgggc 60

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<211> 940

<212> PRT

<213> Homo sapiens

<400> 86

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Leu Arg Leu Ser Phe Ser Glu Ile Asn Thr Arg Val Ile Lys Glu Asp
 35 40 45

Ile Val Arg Arg Glu Arg Ile Gly Phe Arg Val Gln Pro Asp Gln Gly
 50 55 60

Lys Ile Phe Tyr Ser Ser Ile Lys Glu Met Lys Pro Pro Leu Arg Gly
 65 70 75 80

His Gly Lys Gly Ala Trp Gly Lys Glu Asn Val Arg Lys Thr Glu Glu
 85 90 95

Ser Val Leu Lys Val Glu Val Asp Leu Asp Gln Thr Gln Arg Glu Arg
 100 105 110

Lys Met Gln Asn Ala Leu Gly Arg Gly Lys Val Val Pro Leu Trp His
 115 120 125

Pro Ala His Leu Gln Thr Leu Pro Val Thr Pro Asn Lys Gln Lys Thr
 130 135 140

Asp Gly Arg Gly Thr Lys Pro Glu Ala Ser Ser His Gln Gly Thr Pro
 145 150 155 160

Lys Gln Thr Thr Ala Gln Gly Ala Pro Lys Thr Ser Phe Ile Ala Ala
 165 170 175

Lys Gly Thr Gln Val Val Lys Ile Ser Val His Met Gly Arg Val Ser
 180 185 190

Leu Lys Gln Glu Pro Arg Lys Ser His Ser Pro Ser Ser Asp Thr Ser
 195 200 205

Lys Leu Ala Ala Glu Arg Asp Leu Asn Val Thr Ile Ser Leu Ser Thr
 210 215 220

Asp Arg Pro Lys Gln Arg Ser Gln Ala Val Ala Asn Glu Arg Ala His
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Pro Ala Ser Thr Ala Val Pro Lys Ser Gly Glu Ala Met Ala Leu Asn
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Lys Thr Lys Thr Gln Ser Lys Glu Val Asn Ala Asn Lys His Lys Ala
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 His Leu Val Ile Ile Thr Lys Glu Glu Glu Gln Lys Ala Asp Pro Lys
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 Glu Val Ser Asn Ser Lys Thr Lys Thr Ile Phe Pro Lys Val Leu Gly
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 Lys Ser Gln Ser Lys His Ile Ser Arg Asn Arg Ser Glu Met Ser Ser
 355 360 365
 Ser Ser Leu Ala Pro His Arg Val Pro Leu Ser Gln Thr Asn His Ala
 370 375 380
 Leu Thr Gly Gly Leu Glu Pro Ala Lys Ile Asn Ile Thr Ala Lys Ala
 385 390 395 400
 Pro Ser Thr Glu Tyr Asn Gln Ser His Ile Lys Ala Leu Leu Pro Glu
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 Asp Ser Gly Thr His Gln Val Leu Arg Ile Asp Val Thr Leu Ser Pro
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 His Gly Lys Glu Lys Glu Ala Glu Arg Arg Trp Lys Glu Gly Asn Phe
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 Gln Asn Ala Thr Gly Asp Val Leu Thr Phe Leu Asp Ser His Val Glu
 580 585 590

Cys Asn Val Gly Trp Leu Glu Pro Leu Leu Glu Arg Val Tyr Leu Ser
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 Arg Lys Lys Val Ala Cys Pro Val Ile Glu Val Ile Asn Asp Lys Asp
 610 615 620
 Met Ser Tyr Met Thr Val Asp Asn Phe Gln Arg Gly Ile Phe Val Trp
 625 630 635 640
 Pro Met Asn Phe Gly Trp Arg Thr Ile Pro Pro Asp Val Ile Ala Lys
 645 650 655
 Asn Arg Ile Lys Glu Thr Asp Thr Ile Arg Cys Pro Val Met Ala Gly
 660 665 670
 Gly Leu Phe Ser Ile Asp Lys Ser Tyr Phe Phe Glu Leu Gly Thr Tyr
 675 680 685
 Asp Pro Gly Leu Asp Val Trp Gly Gly Glu Asn Met Glu Leu Ser Phe
 690 695 700
 Lys Val Trp Met Cys Gly Gly Glu Ile Glu Ile Ile Pro Cys Ser Arg
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 Val Gly His Ile Phe Arg Asn Asp Asn Pro Tyr Ser Phe Pro Lys Asp
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 740 745 750
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 755 760 765
 Asp Gln Gly Leu Asp Val Gly Asn Leu Thr Gln Gln Arg Glu Leu Arg
 770 775 780
 Lys Lys Leu Lys Cys Lys Ser Phe Lys Trp Tyr Leu Glu Asn Val Phe
 785 790 795 800
 Pro Asp Leu Arg Ala Pro Ile Val Arg Ala Ser Gly Val Leu Ile Asn
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 Val Ala Leu Gly Lys Cys Ile Ser Ile Glu Asn Thr Thr Val Ile Leu
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 Glu Asp Cys Asp Gly Ser Lys Glu Leu Gln Gln Phe Asn Tyr Thr Trp
 835 840 845
 Leu Arg Leu Ile Lys Cys Gly Glu Trp Cys Ile Ala Pro Ile Pro Asp
 850 855 860
 Lys Gly Ala Val Arg Leu His Pro Cys Asp Asn Arg Asn Lys Gly Leu
 865 870 875 880
 Lys Trp Leu His Lys Ser Thr Ser Val Phe His Pro Glu Leu Val Asn
 885 890 895
 His Ile Val Phe Glu Asn Asn Gln Gln Leu Leu Cys Leu Glu Gly Asn
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Phe Ser Gln Lys Ile Leu Lys Val Ala Ala Cys Asp Pro Val Lys Pro
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Tyr Gln Lys Trp Lys Phe Glu Lys Tyr Tyr Glu Ala
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 <212> DNA
 <213> Homo sapiens

<400> 87
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<210> 88
 <211> 286
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Asp Lys Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser Glu Gly Gly
 50 55 60
 Pro Ala Glu Ile Ala Gly Leu Gln Ile Gly Asp Lys Ile Met Gln Val
 65 70 75 80
 Asn Gly Trp Asp Met Thr Met Val Thr His Asp Gln Ala Arg Lys Arg
 85 90 95
 Leu Thr Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val Thr Arg Gln

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210					215					220						
Gly	Ser	Ala	Pro	Ala	Pro	Gln	Pro	Trp	Cys	Val	His	Thr	Ala	Val	Leu	
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<211> 1023

<212> DNA

<213> Homo sapiens

<400> 89

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 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 90
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 35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
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 Gly Tyr Leu Met Gly
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<210> 91
 <211> 3901
 <212> DNA
 <213> Homo sapiens

<400> 91
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a 3901

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<210> 92

<211> 392

<212> PRT

<213> Homo sapiens

<400> 92

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Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu
  1                      5                      10                      15

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Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
 20 25 30
 Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
 35 40 45
 Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
 50 55 60
 Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
 65 70 75 80
 Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
 85 90 95
 Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
 100 105 110
 Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
 115 120 125
 Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
 130 135 140
 Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
 145 150 155 160
 Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
 165 170 175
 His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
 180 185 190
 Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
 195 200 205
 Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
 210 215 220
 Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
 225 230 235 240
 Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
 245 250 255
 Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
 260 265 270
 Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu
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 Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
 290 295 300
 Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
 305 310 315 320
 Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350

Asn Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380

Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 93

<211> 2203

<212> DNA

<213> Homo sapiens

<400> 93

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<210> 94

<211> 674

<212> PRT

<213> Homo sapiens

<400> 94

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Met Trp His Glu Ala Arg Lys His Glu Arg Lys Leu Arg Gly Met Met
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Val Asp Tyr Lys Lys Arg Ala Glu Arg Arg Arg Glu Tyr Tyr Glu Lys
          20           25           30

Ile Lys Lys Asp Pro Ala Gln Phe Leu Gln Val His Gly Arg Ala Cys
          35           40           45

Lys Val His Leu Asp Ser Ala Val Ala Leu Ala Ala Glu Ser Pro Val
          50           55           60

Asn Met Met Pro Trp Gln Gly Asp Thr Asn Asn Met Ile Asp Arg Phe
65           70           75           80

Asp Val Arg Ala His Leu Asp His Ile Pro Asp Tyr Thr Pro Pro Leu
          85           90           95

Leu Thr Thr Ile Ser Pro Glu Gln Glu Ser Asp Glu Arg Lys Cys Asn
          100          105          110

Tyr Glu Arg Tyr Arg Gly Leu Val Gln Asn Asp Phe Ala Gly Ile Ser
          115          120          125

Glu Glu Gln Cys Leu Tyr Gln Ile Tyr Ile Asp Glu Leu Tyr Gly Gly
          130          135          140

Leu Gln Arg Pro Ser Glu Asp Glu Lys Lys Lys Leu Ala Glu Lys Lys
145          150          155          160

Ala Ser Ile Gly Tyr Thr Tyr Glu Asp Ser Thr Val Ala Glu Val Glu
          165          170          175

Lys Ala Ala Glu Lys Pro Glu Glu Glu Glu Ser Ala Ala Glu Glu Glu
          180          185          190

Ser Asn Ser Asp Glu Asp Glu Val Ile Pro Asp Ile Asp Val Glu Val
          195          200          205

Asp Val Asp Glu Leu Asn Gln Glu Gln Val Ala Asp Leu Asn Lys Gln
          210          215          220

Ala Thr Thr Tyr Gly Met Ala Asp Gly Asp Phe Val Arg Met Leu Arg
225          230          235          240

Lys Asp Lys Glu Glu Ala Glu Ala Ile Lys His Ala Lys Ala Leu Glu
          245          250          255

Glu Glu Lys Ala Met Tyr Ser Gly Arg Arg Ser Arg Arg Gln Arg Arg
          260          265          270

Glu Phe Arg Glu Lys Arg Leu Arg Gly Arg Lys Ile Ser Pro Pro Ser
          275          280          285

Tyr Ala Arg Arg Asp Ser Pro Thr Tyr Asp Pro Tyr Lys Arg Ser Pro
          290          295          300

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Ser Glu Ser Ser Ser Glu Ser Arg Ser Arg Ser Arg Ser Pro Thr Pro
 305 310 315 320
 Gly Arg Glu Glu Lys Ile Thr Phe Ile Thr Ser Phe Gly Gly Ser Asp
 325 330 335
 Glu Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Val Thr
 340 345 350
 Thr Gly Lys Pro Pro Ala Pro Pro Gln Pro Gly Gly Pro Ala Pro Gly
 355 360 365
 Arg Asn Ala Ser Ala Arg Arg Arg Ser Ser Ser Ser Ser Ser Ser
 370 375 380
 Ser Ala Ser Arg Thr Ser Ser Ser Arg Ser Ser Ser Arg Ser Ser Ser
 385 390 395 400
 Arg Ser Arg Arg Gly Gly Gly Tyr Tyr Arg Ser Gly Arg His Ala Arg
 405 410 415
 Ser Arg Ser Arg Ser Trp Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr
 420 425 430
 Ser Arg Ser Arg Ser Arg Gly Arg Arg His Ser Gly Gly Gly Ser Arg
 435 440 445
 Asp Gly His Arg Tyr Ser Arg Ser Pro Ala Arg Arg Gly Gly Tyr Gly
 450 455 460
 Pro Arg Arg Arg Ser Arg Ser Arg Ser His Ser Gly Asp Arg Tyr Arg
 465 470 475 480
 Arg Gly Gly Arg Gly Leu Arg His His Ser Ser Ser Arg Ser Arg Ser
 485 490 495
 Ser Trp Ser Leu Ser Pro Ser Arg Ser Arg Ser Leu Thr Arg Ser Arg
 500 505 510
 Ser His Ser Pro Ser Pro Ser Gln Ser Arg Ser Arg Ser Arg Ser Arg
 515 520 525
 Ser Gln Ser Pro Ser Pro Ser Pro Ala Arg Glu Lys Leu Thr Arg Pro
 530 535 540
 Ala Ala Ser Pro Ala Val Gly Glu Lys Leu Lys Lys Thr Glu Pro Ala
 545 550 555 560
 Ala Gly Lys Glu Thr Gly Ala Ala Lys Pro Lys Leu Thr Pro Gln Glu
 565 570 575
 Lys Leu Lys Leu Arg Met Gln Lys Ala Leu Asn Arg Gln Phe Lys Ala
 580 585 590
 Asp Lys Lys Ala Ala Gln Glu Lys Met Ile Gln Gln Glu His Glu Arg
 595 600 605
 Gln Glu Arg Glu Asp Glu Leu Arg Ala Met Ala Arg Lys Ile Arg Met
 610 615 620

Lys Glu Arg Glu Arg Arg Glu Lys Glu Arg Glu Glu Trp Glu Arg Gln
 625 630 635 640

Tyr Ser Arg Gln Ser Arg Ser Pro Ser Pro Arg Tyr Ser Arg Glu Tyr
 645 650 655

Ser Ser Ser Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Pro His Tyr
 660 665 670

Arg His

<210> 95

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 95

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gccatgggag ccgtgactga cgacgaagtt atacggaagc gtctcctcat tgatggagat 180
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gaggctctgg gaaaagaatt agagcatctt tcacacatta aagaaagtgt tgaagataag 600
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<210> 96

<211> 204

<212> PRT

<213> Homo sapiens

<400> 96

Met Gly Ala Val Thr Asp Asp Glu Val Ile Arg Lys Arg Leu Leu Ile
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Asp Gly Asp Gly Ala Gly Asp Asp Arg Arg Ile Asn Leu Leu Val Lys
 20 25 30

Ser Phe Ile Lys Trp Cys Asn Ser Gly Ser Gln Glu Glu Gly Tyr Ser
 35 40 45

Gln Tyr Gln Arg Met Leu Ser Thr Leu Ser Gln Cys Glu Phe Ser Met
 50 55 60

Gly Lys Thr Leu Leu Val Tyr Asp Met Asn Leu Arg Glu Met Glu Asn
 65 70 75 80

Tyr Glu Lys Ile Tyr Lys Glu Ile Glu Cys Ser Ile Ala Gly Ala His
 85 90 95

Glu Lys Ile Ala Glu Cys Lys Lys Gln Ile Leu Gln Ala Lys Arg Ile
 100 105 110
 Arg Lys Asn Arg Gln Glu Tyr Asp Ala Leu Ala Lys Val Ile Gln His
 115 120 125
 His Pro Asp Arg His Glu Thr Leu Lys Glu Leu Glu Ala Leu Gly Lys
 130 135 140
 Glu Leu Glu His Leu Ser His Ile Lys Glu Ser Val Glu Asp Lys Leu
 145 150 155 160
 Glu Leu Arg Arg Lys Gln Phe His Val Leu Leu Ser Thr Ile His Glu
 165 170 175
 Leu Gln Gln Thr Leu Glu Asn Asp Glu Lys Leu Ser Glu Val Glu Glu
 180 185 190
 Ala Gln Glu Ala Ser Met Glu Thr Asp Pro Lys Pro
 195 200

<210> 97
 <211> 955
 <212> DNA
 <213> Homo sapiens

<400> 97
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 acagagagaa gagaagagga agatattgaa gagaagaaat cgattaagaa aaaaattaaa 660
 gaacttaagt ttttagattc taaaattgcc cagaaccttt gtaagtatca tattccaata 720
 ccattcaagg acagtggaaa tttttcttta aatgatttca ttttcttta gaccgattat 780
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<210> 98
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 98
 Met Ile Lys Ser Ser Leu Phe Pro Leu Leu Tyr Leu Asn Glu Leu Leu
 1 5 10 15
 Pro Leu Thr Trp Ile Tyr Leu Gly Phe Thr Glu Arg Arg Glu Glu Glu
 20 25 30
 Asp Ile Glu Glu Lys Lys Ser Ile Lys Lys Lys Ile Lys Glu Leu Lys
 35 40 45

Phe Leu Asp Ser Lys Ile Ala Gln Asn Leu Cys Lys Tyr His Ile Pro
 50 55 60

Ile Pro Phe Lys Asp Ser Gly Asn Ile Ser Leu Asn Asp Phe Ile Phe
 65 70 75 80

Phe Lys Thr Asp Tyr Ser Leu Phe Ala Ile Phe Ile Leu Leu Leu Tyr
 85 90 95

Ala

<210> 99

<211> 1375

<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 132

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Glu Thr Val Lys Ala Pro Leu Asp Ser Gly Lys Ala Phe Ile
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Thr Phe Thr Pro Leu Pro Leu Pro Ser Pro Ala Ser Arg Pro Glu Gly
 20 25 30

Cys Arg Gly Ser Trp Gln Leu Leu Gly Glu Val Ser Trp His Arg Leu
 35 40 45

Thr Leu Leu Ser Gly Thr Thr Ser Phe Pro Phe Glu Glu Thr Ala Thr

50

55

60

Ala Val Ala Lys Ala Ala Ala Pro Ala Met Arg Val Tyr Ile Phe
65 70 75 80

Phe Thr Gln Ser Ser Gly Ile Val His Leu Phe Phe Lys Thr Gln Arg
85 90 95

Gly Lys Glu Pro Cys Ile Ile Cys Glu His Cys Ile Ile Gly Asn Val
100 105 110

Val Gln Thr Leu Leu Tyr Ser Asp Leu Ser Cys Ser Cys Ser Lys Asn
115 120 125

Pro Leu Trp Thr
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<210> 101

<211> 1213

<212> DNA

<213> Homo sapiens

<400> 101

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aaaaaaaaaa aaa 1213

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<210> 102

<211> 100

<212> PRT

<213> Homo sapiens

<400> 102

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Met Lys Gly Val His His Arg Pro His Glu Ala Val Pro Thr Trp Ala
  1           5           10           15

Cys Gly Trp Gly Val Ala Thr Thr Glu His Met Ala Val Ser Arg Arg
          20           25           30

Lys His Phe Ser Ser Ile Cys Leu His Ala Gln Gly Ser Ser Arg Leu
    35           40           45

```

Pro Val Leu Ser Thr Gly Thr Ala Val Ser Glu Leu Leu Arg Thr Ser
 50 55 60

Leu Cys Gln Val Val Glu Leu Gly Pro Ser Pro Tyr Leu Ser Leu Val
 65 70 75 80

Pro Thr Val Leu Leu Thr Val Gln His Leu Gly Ala Leu Ala Trp Gly
 85 90 95

Trp Arg Pro Trp
 100

<210> 103

<211> 1036

<212> DNA

<213> Homo sapiens

<400> 103

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taatgtagct tcaaaaaataa aatgtgtctat ttatatgaca tgaaattcat aacttttgga 660
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gcctatatac ttacaaagta ttcaatgtgt acttagcggc gcttaaaata tgtcatgtac 900
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aaaaaaaaaa aaaaaa 1036
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<210> 104

<211> 87

<212> PRT

<213> Homo sapiens

<400> 104

Met Tyr Thr Ile Leu Ile Phe Leu Gln Ile Tyr Leu Thr Val Pro Thr
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Val Leu Ile Val Asp Ser Met Thr Gln Leu Ser His His Pro Arg Ile
 20 25 30

Tyr Glu Phe Glu Ile Thr Asp Leu Phe Ser Ser Tyr Cys Ile His Ile
 35 40 45

Asn Ile Cys Glu Phe Val Val Gln Leu Phe Ile Gln Thr Lys Asn Ile
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Pro Ser Arg Lys Leu His Phe Tyr His Lys His Phe Asn Ile Thr Asn
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Ile Arg Thr Ser Leu Pro Cys

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<210> 105

<211> 2349

<212> DNA

<213> Homo sapiens

<400> 105

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<210> 106

<211> 539

<212> PRT

<213> Homo sapiens

<400> 106

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 65 70 75 80
 Leu Thr Met Ser Gln Asp Gly Phe Pro Asn Glu Asp Gly Glu Gln Met
 85 90 95
 Thr Pro Glu Leu Leu Leu Gln Glu Arg Gln Arg Ala Ser Glu Trp
 100 105 110
 Pro Lys Asp Arg Val Leu Ile Asn Arg Ile Asp Leu Val Cys Gln Ala
 115 120 125
 Val Leu Ser Gly Lys Trp Pro Ser Ser Arg Arg Ser Gln Glu Met Val
 130 135 140
 Thr Gly Gly Ile Leu Gly Pro Gly Asn His Leu Leu Asp Ser Pro Ser
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 Leu Thr Pro Gly Glu Tyr Gly Asp Ser Pro Val Pro Thr Pro Arg Ser
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 Ala Ala Ala Gln Phe Thr Lys Leu Arg Arg Gly Met Asp Glu Lys Glu
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 Phe Thr Val Gln Ile Lys Asp Glu Glu Gly Leu Lys Leu Thr Phe Gln
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 Lys His Lys Leu Met Ala Asn Gly Val Met Gly Asp Gly His Pro Leu
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 Phe His Lys Lys Lys Gly Asn Arg Lys Lys Leu Val Glu Leu Glu Val
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 Glu Cys Met Glu Glu Pro Asn His Leu Asp Val Asp Leu Glu Thr Arg
 260 265 270
 Ile Pro Val Ile Asn Lys Val Asp Gly Thr Leu Leu Val Gly Glu Asp
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 Ala Pro Arg Arg Ala Glu Leu Glu Met Trp Leu Gln Gly His Pro Glu
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 325 330 335

Leu Gly Met Glu Pro Val Gln Thr Ala Asn Ser Arg Asn Gly Lys Lys
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 Gly His His Thr Glu Thr Val Phe Asn Arg Val Leu Pro Gly Pro Ile
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 Ser Lys Met Met Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser
 385 390 395 400
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 405 410 415
 Ser Leu Gly His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro
 420 425 430
 Phe Val Met Gly Gly Ala Pro Ser Ser Pro His Val Asp Ser Ser Thr
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 Met Leu His His His His His His Pro His Pro His His His His His
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 His His Pro Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr
 465 470 475 480
 Thr Ala Ser Gly Thr Thr Leu Arg Leu Pro Pro Leu Gln Pro Glu Glu
 485 490 495
 Asp Asp Asp Glu Asp Glu Glu Asp Asp Asp Asp Leu Ser Gln Gly Tyr
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<210> 107

<211> 3004

<212> DNA

<213> Homo sapiens

<400> 107

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<210> 108

<211> 959

<212> PRT

<213> Homo sapiens

<400> 108

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Arg Phe Trp Gly Pro Trp Pro Leu Leu Thr Trp Gln Leu Leu Ser Leu
      20             25             30

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Leu Val Lys Glu Ala Gln Pro Leu Val Trp Val Lys Asp Pro Leu Gln
      35             40             45

```

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Leu Thr Ser Asn Pro Leu Gly Pro Pro Glu Pro Trp Ser Ser Arg Ser
      50             55             60

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Ser His Leu Pro Trp Glu Ser Pro His Ala Pro Ala Pro Pro Ala Ala
      65             70             75             80

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Pro Gly Asp Phe Asp Tyr Leu Gly Pro Ser Ala Ser Ser Gln Met Ser

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Ala	His	Gln	Asp	Leu	Asn	Asp	Lys	Arg	Thr	Pro	Glu	Glu	Arg	Leu	Pro				
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Glu	Val	Val	Pro	Leu	Leu	Asn	Arg	Asp	Gln	Asn	Gln	Ala	Leu	Val	Gln				
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Gly	His	Gln	Ala	Asp	Glu	Ile	Leu	Val	Pro	Leu	Asp	Ser	Lys	Val	Ser				
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Arg	Pro	Thr	Lys	Phe	Val	Val	Ser	Pro	Lys	Asn	Leu	Lys	Lys	Asp	Leu				
		195					200					205							
Ala	Glu	Arg	Trp	Ser	Leu	Pro	Glu	Ile	Val	Gly	Ile	Pro	His	Gln	Leu				
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Glu	Ser	Ser	Met	Glu	Ser	Leu	Ala	Gln	Thr	Pro	Leu	Asn	His	Glu	Val				
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Thr	Val	Gln	Pro	Pro	Gly	Glu	Asp	Gln	Ala	His	Tyr	Asn	Leu	Pro	Lys				
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Phe	Thr	Val	Lys	Pro	Ala	Asp	Val	Glu	Val	Thr	Met	Thr	Ser	Glu	Pro				
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Pro	Pro	Glu	Glu	Ala	Glu	Pro	Ser	Ser	Thr	Ala	Leu	Arg	Thr	Thr	Asp				
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Pro Thr Thr Glu Glu Thr Ser	Ala Gln Pro Pro Asp Pro Gly Leu Ala				
450	455	460			
Ile Thr Pro Glu Pro Thr Thr	Glu Ile Gly His Ser Thr Ala Leu Glu				
465	470	475	480		
Lys Thr Arg Ala Pro His Pro Asp	Gln Val Gln Thr Leu His Arg Ser				
485	490	495			
Leu Thr Glu Val Thr Gly Pro Pro	Thr Lys Leu Glu Ser Ser Gln Asp				
500	505	510			
Ser Leu Val Gln Ser Glu Thr	Ala Pro Glu Glu Gln Lys Ala Ser Thr				
515	520	525			
Ser Thr Asn Ile Cys Glu Leu Cys	Thr Cys Gly Asp Glu Thr Leu Ser				
530	535	540			
Cys Val Gly Leu Ser Pro Lys Gln	Arg Leu Arg Gln Val Pro Val Pro				
545	550	555	560		
Glu Pro Asp Thr Tyr Asn Gly	Ile Phe Thr Thr Leu Asn Phe Gln Gly				
565	570	575			
Asn Tyr Ile Ser Tyr Leu Asp	Gly Asn Val Trp Lys Ala Tyr Ser Trp				
580	585	590			
Thr Glu Lys Leu Ile Leu Ser	Glu Asn Tyr Leu Thr Glu Leu Pro Lys				
595	600	605			
Asp Ser Phe Glu Gly Leu Leu	Tyr Leu Gln Tyr Leu Asp Leu Ser Cys				
610	615	620			
Asn Lys Ile Arg Tyr Ile Glu	Arg Gln Thr Phe Glu Ser Leu Pro Phe				
625	630	635	640		
Leu Gln Tyr Ile Asn Leu Gly	Cys Asn Leu Ile Thr Lys Leu Ser Leu				
645	650	655			
Gly Thr Phe Gln Ala Trp His	Gly Met Gln Phe Leu His Asn Leu Ile				
660	665	670			
Leu Asn Arg Asn Pro Leu Thr	Thr Val Glu Asp Pro Tyr Leu Phe Glu				
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Leu Pro Ala Leu Lys Tyr Leu	Asp Met Gly Thr Thr His Ile Thr Leu				
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Thr Thr Leu Lys Asn Ile Leu	Thr Met Thr Val Glu Leu Glu Lys Leu				
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Ile Leu Pro Ser His Met Ala	Cys Cys Leu Cys Gln Phe Lys Asn Ser				

725										730					735				
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Leu	Thr	Asn	Ser	Ile	His	Cys	Pro	Glu	Glu	Ala	Ser	Val	Gly	Asn	Pro				
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Thr	Gln	Leu	Thr	Ile	Glu	Ser	Glu	Ala	Pro	Ser	Asp	Ser	Ser	Gly	Ile				
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Asn	Leu	Ser	Gly	Phe	Gly	Gly	Asp	Gln	Leu	Glu	Ile	Gln	Leu	Thr	Glu				
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Gln	Leu	Arg	Ser	Leu	Ile	Pro	Asn	Glu	Asp	Val	Arg	Lys	Phe	Met	Ser				
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His	Val	Ile	Arg	Thr	Leu	Lys	Met	Glu	Cys	Ser	Glu	Thr	His	Val	Gln				
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Gly	Ser	Cys	Ala	Lys	Leu	Met	Ser	Arg	Thr	Gly	Leu	Leu	Met	Lys	Leu				
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Leu	Ser	Glu	Gln	Gln	Glu	Ala	Lys	Ala	Leu	Asn	Val	Glu	Trp	Asp	Thr				
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				885					890					895					
Gln	Lys	Glu	Gln	Lys	Ser	Ser	Glu	Leu	Met	Lys	Glu	Val	Pro	Gly	Asp				
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Asp	Tyr	Lys	Asn	Lys	Leu	Ile	Phe	Ala	Ile	Ser	Val	Thr	Val	Ile	Leu				
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<210> 109

<211> 1331

<212> DNA

<213> Homo sapiens

<400> 109

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1331

<210> 110

<211> 118

<212> PRT

<213> Homo sapiens

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Gly Gly Glu Val Ala Tyr Gly Gln Val Leu Gly Val Ile Gly Tyr Ser
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Leu Leu Pro Leu Ile Val Ile Ala Pro Val Leu Leu Val Val Gly Ser
          50             55             60
Phe Glu Val Val Ser Thr Leu Ile Lys Leu Phe Gly Val Phe Trp Ala
          65             70             75             80
Ala Tyr Ser Ala Ala Ser Leu Leu Val Gly Glu Glu Phe Lys Thr Lys
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Lys Pro Leu Leu Ile Tyr Pro Ile Phe Leu Leu Tyr Ile Tyr Phe Leu
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Ser Leu Tyr Thr Gly Val
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<210> 111

<211> 2610

<212> DNA

<213> Homo sapiens

<400> 111

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<210> 112

<211> 116

<212> PRT

<213> Homo sapiens

<400> 112

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Leu Ser Leu Tyr Thr His Val Thr Cys Ser Ser Leu Pro Ser Ser Leu
      20             25             30

Cys Leu Tyr Ile Tyr Tyr Tyr His Arg Gly Leu Gly Lys Lys Thr Pro
      35             40             45

Thr Ala Ala Pro His Thr His Pro Pro Ala Leu Tyr His Leu Leu Cys
      50             55             60

Phe Val Phe Leu Cys Arg Ile His Asp Phe Leu Lys Tyr Asn Phe Phe
      65             70             75             80

Asn Val Tyr Ile Leu Tyr Ala Phe Ser His Ser Tyr Val Lys Ser Gly
      85             90             95

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Arg His Arg Leu Val Phe Leu Phe Thr Val Asp Ala Ser Val Pro Lys
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Ile Cys Ile Ala
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<210> 113
 <211> 2759
 <212> DNA
 <213> Homo sapiens

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<210> 114
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 114
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 His Ala Met Arg Arg Leu Ile Asn Leu Leu Arg Gln Ser Gln Ser Tyr
 20 25 30
 Cys Thr Asp Thr Glu Cys Leu Gln Glu Leu Pro Gly Pro Ser Gly Asp
 35 40 45
 Asn Gly Ile Ser Val Thr Met Ile Leu Val Ala Trp Met Val Ile Ala
 50 55 60
 Leu Ile Leu Phe Leu Leu Arg Pro Pro Asn Leu Arg Gly Ser Ser Leu
 65 70 75 80
 Pro Gly Lys Pro Thr Ser Pro His Asn Gly Gln Asp Pro Pro Ala Pro
 85 90 95
 Pro Val Asp

<210> 115
 <211> 1404
 <212> DNA
 <213> Homo sapiens

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<210> 116
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 116

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Met Ser Trp Val Pro Gly Val Gly Met Glu Ile Arg Gly Glu Pro Gly
 1              5              10              15

Ser Ala Leu Thr Pro Leu Trp Ser Pro Tyr Pro Ala Gly Phe Leu Leu
      20              25              30

Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu
      35              40              45

Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu
      50              55              60

Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu
      65              70              75              80

Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val
      85              90              95

Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu
      100             105             110

Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser
      115             120             125

His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys
      130             135             140

Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser
      145             150             155             160

Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly
      165             170             175

Leu Ala Leu Glu Ile Arg Ser Leu
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<210> 117
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 <213> Homo sapiens

<400> 117

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<210> 118

<211> 86

<212> PRT

<213> Homo sapiens

<400> 118

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Met Val Arg Lys Val Asn Ala His Leu Pro Leu Ser Phe Pro Thr Val
  1                      5                      10                      15

```

```

Glu Thr Asp Ser Arg Glu Ile Leu Gln Val Arg Cys Tyr Val Gly Leu
          20                      25                      30

```

```

Arg Glu Arg Cys Tyr Asp Gln Thr Glu Pro Phe Ser Leu Pro Ser Val
          35                      40                      45

```

```

His Gly Phe Ser Trp Leu Cys Gly Pro Val Ser Cys His Ser Phe Thr
          50                      55                      60

```

```

Pro Asn Phe Trp Asp Ile Gln Gly Asn Asn Leu Ala Thr Gly Tyr Leu
          65                      70                      75                      80

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Leu Val Glu Ile Met Trp
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<210> 119

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 119

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29

<210> 120

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 120

cncacagaaa attcaataag accctcgct

29

<210> 121

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 121

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<210> 122

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 122

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29

<210> 123

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)
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<210> 124
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
<223> biotinylated phosphoramidite residue

<400> 124
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<210> 125
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
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<400> 125
ancggcaggg aacttacagg gacagagct 29

<210> 126
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
<223> biotinylated phosphoramidite residue

<400> 126
nggttttcgg tgatgatggt gtagaggat 29

<210> 127
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

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<222> (2)

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<400> 127

cnagaacaca tagggatgcg agagcaagc

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<210> 128

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 128

anactgaaaa ctgagtatgt gcgagtgtgta

29

<210> 129

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 129

gntatccatt tcctcttctt catctgagt

29

<210> 130

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

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<222> (2)

<223> biotinylated phosphoramidite residue

<400> 130

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29

<210> 131

<211> 29

<212> DNA
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<400> 131
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<210> 132
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (2)
<223> biotinylated phosphoramidite residue

<400> 132
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<210> 133
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
<223> biotinylated phosphoramidite residue

<400> 133
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<210> 134
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
<223> biotinylated phosphoramidite residue

<400> 134

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29

<210> 135

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 135

cncagaagca gaagaatgac aggcaacac

29

<210> 136

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

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<210> 137

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

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<220>

<221> misc_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 137

gnccagaaaag ttgaggacat gctgggcag

29

<210> 138

<211> 29

<212> DNA

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35 40 45
Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu
50 55 60
Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys
65 70 75 80
Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val
85 90 95
Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu
100 105 110
Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu
115 120 125
Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His
130 135 140
Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro
145 150 155 160
Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys
165 170 175
Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly
180 185 190
His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe
195 200 205
Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val
210 215 220
Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys
225 230 235 240
Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln
245 250 255
Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr
260 265 270

Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg
 275 280 285
 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe
 290 295 300
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp
 305 310 315 320
 Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn
 325 330 335
 Thr Lys Val Ala Lys Leu Thr Asn Glu Leu Lys Glu Glu Gln Glu Met
 340 345 350
 Asn Lys Cys Leu Arg Ala Asn Gln Val Leu Leu Gln Asn Lys Leu Lys
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 50 55 60
 Phe Leu Trp Gly Cys Asn Leu Leu Ala His Phe Ile Asn Ala Tyr Leu
 65 70 75 80
 Val Asp Asp Ser Phe Ser Gln Ala Leu Ala Ile Arg Ser Tyr Thr Lys
 85 90 95
 Phe Val Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu
 100 105 110
 Val Gly Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu
 115 120 125
 Pro Pro Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr
 130 135 140
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 Glu Leu Leu Leu Leu Leu Leu His Leu Gln Trp Gly Leu Gly Leu Leu
 35 40 45
 Arg Gln Leu His His Lys Arg Leu Ala Gln Leu Leu Leu His Arg Arg
 50 55 60
 Arg Asp His Pro Ile Pro Pro Ile Gln Asp Ile Leu Gly Ile Ala Lys
 65 70 75 80
 Cys Pro Cys Pro Trp Ala Ile Ile Leu Met Arg Met Ala Ser Ile Ile
 85 90 95
 Cys His Ile His Gln Cys Ile Thr Arg Val Leu Asp Arg Leu His Thr
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 20 25 30
 His Leu Leu Pro Cys Ser Val Ser Ser Leu Ser Pro Arg Leu Ala Gln
 35 40 45
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 50 55 60
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 65 70 75 80

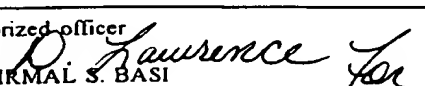
WO 99/57132

PCT/US99/09970

Leu Ala

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/09970

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) :C07H 21/04; C07K 14/705; C12N 15/09, 15/63; C12Q 1/68 US CL :Please See Extra Sheet. According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 536/23.1, 24.3; 435/7.2, 69.1; 530/350 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) GENEMBL,N-GENSEQ-34,EST,A-GENSEQ35,PIR60,SWISS-PROT37,SPTREMBL19,APS,MEDLINE,CAPLUS,WPIDS, JAPIO, SCISEARCH Search terms: secreted protein, bn36553,gage 1, gage 6, rgd		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	Database EST, Accession Number AA242967, HILLIER, L. et al. WashU_Merck EST Project 1997, 06 August 1997.	1-3 ----- 4-7, 9, 11
X - Y	Database EST, Accession Number AA524997, NCI-CGAP http://www.nci.nlm.nih.gov/ncicgap , National cancer Institute, cancer Genome AnDatomy Project (CGAP), Tumor Gene Index. 05 August 1997.	1-3 ----- 4-7, 9, 11
X,P --- Y,P	Database Sptrembl19, Accession Number 060829, STROM, T. M et al. JM27 Protein, Complete CDs (Clone Image 145745 and Image 257878), 01 August 1998.	1-3 ----- 4-7, 9, 11
X,P --- Y,P	Database GenEmbl, Accession Number HSA005894, AJ005894, STROM, T. M. et al. Transcription map in Hp11.23, 15 May 1998.	1-3 ----- 4-7, 9, 11
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed		"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family
Date of the actual completion of the international search 22 JULY 1999		Date of mailing of the international search report 09 SEP 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer  NIKMAL S. BASU Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/09970

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ROBINSON, A.K. et al. A Gene from the Hyperthermophile <i>Pyrococcus furiosus</i> whose Deduced Product is Homologous to Members of the Prolyl Oligopeptidase Family of Proteases. <i>Gene</i> . 1995, Vol. 152, pages 103-106, see Fig. 1, amino acids 358-365.	9, 11
Y	BERGER, S.L. et al. Guide to Molecular Cloning Techniques. <i>Methods in Enzymology</i> . 1987, Vol. 152, pages 661-673, see entire document.	1-7, 9, 11

Form PCT/ISA/210 (continuation of second sheet)(July 1992)★

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/09970

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/09970

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

536/23.1, 24.3; 435/7.2, 69.1; 530/350

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-11, drawn to polynucleotide comprising SEQ ID NO:1, fragments thereof, expression vector containing said sequence, cell transformed with said vector, polypeptide of SEQ ID NO:2, fragments of the polypeptide of SEQ ID NO:2, process for preparing said polypeptide.

Group II, claim(s)12-13, drawn to polynucleotides comprising SEQ ID NO:3, fragments thereof, polypeptide of SEQ ID NO:4, fragments of the polypeptide of SEQ ID NO:4.

Group III, claim(s)14-15, drawn to polynucleotides comprising SEQ ID NO:5, fragments thereof, polypeptide of SEQ ID NO:6, fragments of the polypeptide of SEQ ID NO:6.

Group IV, claim(s)16-17, drawn to polynucleotides comprising SEQ ID NO:7, fragments thereof, polypeptide of SEQ ID NO:8, fragments of the polypeptide of SEQ ID NO:8.

Group V, claim(s)18-19, drawn to polynucleotides comprising SEQ ID NO:9, fragments thereof, polypeptide of SEQ ID NO:10, fragments of the polypeptide of SEQ ID NO:10.

Group VI, claim(s)20-21, drawn to polynucleotides comprising SEQ ID NO:11, fragments thereof, polypeptide of SEQ ID NO:12, fragments of the polypeptide of SEQ ID NO:12.

Group VII, claim(s)22-23, drawn to polynucleotides comprising SEQ ID NO:13, fragments thereof, polypeptide of SEQ ID NO:14, fragments of the polypeptide of SEQ ID NO:14.

Group VIII, claim(s)24-25, drawn to polynucleotides comprising SEQ ID NO:15, fragments thereof, polypeptide of SEQ ID NO:16, fragments of the polypeptide of SEQ ID NO:16.

Group IX, claim(s)26-27, drawn to polynucleotides comprising SEQ ID NO:17, fragments thereof, polypeptide of SEQ ID NO:18, fragments of the polypeptide of SEQ ID NO:18.

Group X, claim(s)28-29, drawn to polynucleotides comprising SEQ ID NO:19, fragments thereof, polypeptide of SEQ ID NO:20, fragments of the polypeptide of SEQ ID NO:20.

Group XI, claim(s)30-31, drawn to polynucleotides comprising SEQ ID NO:21, fragments thereof, polypeptide of SEQ ID NO:22, fragments of the polypeptide of SEQ ID NO:22.

Group XII, claim(s)32-33, drawn to polynucleotides comprising SEQ ID NO:23, fragments thereof, polypeptide of SEQ ID NO:24, fragments of the polypeptide of SEQ ID NO:24.

Group XIII, claim(s)34-35, drawn to polynucleotides comprising SEQ ID NO:25, fragments thereof, polypeptide of SEQ ID NO:26, fragments of the polypeptide of SEQ ID NO:26.

Group XIV, claim(s)36-37, drawn to polynucleotides comprising SEQ ID NO:27, fragments thereof, polypeptide of SEQ ID NO:28, fragments of the polypeptide of SEQ ID NO:28.

Group XV, claim(s)38-39, drawn to polynucleotides comprising SEQ ID NO:29, fragments thereof, polypeptide of SEQ ID NO:30, fragments of the polypeptide of SEQ ID NO:30.

Group XVI, claim(s)40-41, drawn to polynucleotides comprising SEQ ID NO:31, fragments thereof, polypeptide of SEQ ID NO:32, fragments of the polypeptide of SEQ ID NO:32.

Group XVII, claim(s)42-43, drawn to polynucleotides comprising SEQ ID NO:33, fragments thereof, polypeptide of SEQ ID NO:34, fragments of the polypeptide of SEQ ID NO:34.

Group XVIII, claim(s)44-45, drawn to polynucleotides comprising SEQ ID NO:35, fragments thereof, polypeptide of SEQ ID NO:36, fragments of the polypeptide of SEQ ID NO:36.

Group XIX, claim(s)46-47, drawn to polynucleotides comprising SEQ ID NO:37, fragments thereof, polypeptide of SEQ ID NO:38, fragments of the polypeptide of SEQ ID NO:38.

Group XX, claim(s)48-49, drawn to polynucleotides comprising SEQ ID NO:39, fragments thereof, polypeptide of SEQ ID NO:40, fragments of the polypeptide of SEQ ID NO:40.

Group XXI, claim(s)50-51, drawn to polynucleotides comprising SEQ ID NO:41, fragments thereof, polypeptide of SEQ ID NO:42, fragments of the polypeptide of SEQ ID NO:42.

Group XXII, claim(s)52-53, drawn to polynucleotides comprising SEQ ID NO:43, fragments thereof, polypeptide of SEQ ID NO:44, fragments of the polypeptide of SEQ ID NO:44.

Group XXIII, claim(s)54-55, drawn to polynucleotides comprising SEQ ID NO:45, fragments thereof, polypeptide of SEQ ID NO:46, fragments of the polypeptide of SEQ ID NO:46.

Group XXIV, claim(s)56-57, drawn to polynucleotides comprising SEQ ID NO:47, fragments thereof,

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polypeptide of SEQ ID NO:48, fragments of the polypeptide of SEQ ID NO:48.

Group XXV, claim(s)58-59, drawn to polynucleotides comprising SEQ ID NO:49, fragments thereof, polypeptide of SEQ ID NO:50, fragments of the polypeptide of SEQ ID NO:50.

Group XXVI, claim(s)60-61, drawn to polynucleotides comprising SEQ ID NO:51, fragments thereof, polypeptide of SEQ ID NO:52, fragments of the polypeptide of SEQ ID NO:52.

Group XXVII, claim(s)62-63, drawn to polynucleotides comprising SEQ ID NO:53, fragments thereof, polypeptide of SEQ ID NO:54, fragments of the polypeptide of SEQ ID NO:54.

Group XXVIII, claim(s)64-65, drawn to polynucleotides comprising SEQ ID NO:55, fragments thereof, polypeptide of SEQ ID NO:56, fragments of the polypeptide of SEQ ID NO:56.

Group XXIX, claim(s)66-67, drawn to polynucleotides comprising SEQ ID NO:57, fragments thereof, polypeptide of SEQ ID NO:58, fragments of the polypeptide of SEQ ID NO:58.

Group XXX, claim(s)68-69, drawn to polynucleotides comprising SEQ ID NO:59, fragments thereof, polypeptide of SEQ ID NO:60, fragments of the polypeptide of SEQ ID NO:60.

Group XXXI, claim(s)70-71, drawn to polynucleotides comprising SEQ ID NO:61, fragments thereof, polypeptide of SEQ ID NO:62, fragments of the polypeptide of SEQ ID NO:62.

Group XXXII, claim(s)72-73, drawn to polynucleotides comprising SEQ ID NO:63, fragments thereof, polypeptide of SEQ ID NO:64, fragments of the polypeptide of SEQ ID NO:64.

Group XXXIII, claim(s)74-75, drawn to polynucleotides comprising SEQ ID NO:65, fragments thereof, polypeptide of SEQ ID NO:66, fragments of the polypeptide of SEQ ID NO:66.

Group XXXIV, claim(s)76-77, drawn to polynucleotides comprising SEQ ID NO:67, fragments thereof, polypeptide of SEQ ID NO:68, fragments of the polypeptide of SEQ ID NO:68.

Group XXXV, claim(s)78-79, drawn to polynucleotides comprising SEQ ID NO:69, fragments thereof, polypeptide of SEQ ID NO:70, fragments of the polypeptide of SEQ ID NO:70.

Group XXXVI, claim(s)80-81, drawn to polynucleotides comprising SEQ ID NO:71, fragments thereof, polypeptide of SEQ ID NO:72, fragments of the polypeptide of SEQ ID NO:72.

Group XXXVII, claim(s)82-83, drawn to polynucleotides comprising SEQ ID NO:73, fragments thereof, polypeptide of SEQ ID NO:74, fragments of the polypeptide of SEQ ID NO:74.

Group XXXVIII, claim(s)84-85, drawn to polynucleotides comprising SEQ ID NO:75, fragments thereof, polypeptide of SEQ ID NO:76, fragments of the polypeptide of SEQ ID NO:76.

Group XXXIX, claim(s)86-87, drawn to polynucleotides comprising SEQ ID NO:77, fragments thereof, polypeptide of SEQ ID NO:78, fragments of the polypeptide of SEQ ID NO:78.

Group XL, claim(s)88-89, drawn to polynucleotides comprising SEQ ID NO:79, fragments thereof, polypeptide of SEQ ID NO:80, fragments of the polypeptide of SEQ ID NO:80.

Group XLI, claim(s)90-91, drawn to polynucleotides comprising SEQ ID NO:81, fragments thereof, polypeptide of SEQ ID NO:82, fragments of the polypeptide of SEQ ID NO:82.

Group XLII, claim(s)92-93, drawn to polynucleotides comprising SEQ ID NO:83, fragments thereof, polypeptide of SEQ ID NO:84, fragments of the polypeptide of SEQ ID NO:84.

Group XLIII, claim(s)94-95, drawn to polynucleotides comprising SEQ ID NO:85, fragments thereof, polypeptide of SEQ ID NO:86, fragments of the polypeptide of SEQ ID NO:86.

Group XLIV, claim(s)96-97, drawn to polynucleotides comprising SEQ ID NO:87, fragments thereof, polypeptide of SEQ ID NO:88, fragments of the polypeptide of SEQ ID NO:88.

Group XLV, claim(s)98-99, drawn to polynucleotides comprising SEQ ID NO:89, fragments thereof, polypeptide of SEQ ID NO:90, fragments of the polypeptide of SEQ ID NO:90.

Group XLVI, claim(s)100-101, drawn to polynucleotides comprising SEQ ID NO:91, fragments thereof, polypeptide of SEQ ID NO:92, fragments of the polypeptide of SEQ ID NO:92.

Group XLVII, claim(s)102-103, drawn to polynucleotides comprising SEQ ID NO:93, fragments thereof, polypeptide of SEQ ID NO:94, fragments of the polypeptide of SEQ ID NO:94.

Group XLVIII, claim(s)104-105, drawn to polynucleotides comprising SEQ ID NO:95, fragments thereof, polypeptide of SEQ ID NO:96, fragments of the polypeptide of SEQ ID NO:96.

Group XLIX, claim(s)106-107, drawn to polynucleotides comprising SEQ ID NO:97, fragments thereof, polypeptide of SEQ ID NO:98, fragments of the polypeptide of SEQ ID NO:98.

Group L, claim(s)108-109, drawn to polynucleotides comprising SEQ ID NO:99, fragments thereof, polypeptide of SEQ ID NO:100, fragments of the polypeptide of SEQ ID NO:100.

Group LI, claim(s)110-111, drawn to polynucleotides comprising SEQ ID NO:101, fragments thereof, polypeptide of SEQ ID NO:102, fragments of the polypeptide of SEQ ID NO:102.

Group LII, claim(s)112-113, drawn to polynucleotides comprising SEQ ID NO:103, fragments thereof, polypeptide of SEQ ID NO:104, fragments of the polypeptide of SEQ ID NO:104.

Group LIII, claim(s)114-115, drawn to polynucleotides comprising SEQ ID NO:105, fragments thereof, polypeptide of SEQ ID NO:106, fragments of the polypeptide of SEQ ID NO:106.

Group LIV, claim(s)116-117, drawn to polynucleotides comprising SEQ ID NO:107, fragments thereof, polypeptide of SEQ ID NO:108, fragments of the polypeptide of SEQ ID NO:108.

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Group LV, claim(s)118-119, drawn to polynucleotides comprising SEQ ID NO:109, fragments thereof, polypeptide of SEQ ID NO:110, fragments of the polypeptide of SEQ ID NO:110.

Group LVI, claim(s)120-121, drawn to polynucleotides comprising SEQ ID NO:111, fragments thereof, polypeptide of SEQ ID NO:112, fragments of the polypeptide of SEQ ID NO:112

Group LVII, claim(s)122-123, drawn to polynucleotides comprising SEQ ID NO:113, fragments thereof, polypeptide of SEQ ID NO:114, fragments of the polypeptide of SEQ ID NO:114.

Group LVIII, claim(s)124-125, drawn to polynucleotides comprising SEQ ID NO:115, fragments thereof, polypeptide of SEQ ID NO:116, fragments of the polypeptide of SEQ ID NO:116.

Group LVIII, claim(s)126-127, drawn to polynucleotides comprising SEQ ID NO:117, fragments thereof, polypeptide of SEQ ID NO:118, fragments of the polypeptide of SEQ ID NO:118.

The inventions listed as Groups I-LVIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The main invention is Group I, which is first product, first method of making the product and first method of using the product. Pursuant to 37 CFR 1.474 (d), these claims are considered by the ISA/US to constitute the main invention and none of the related Groups II-LVIII correspond to the main invention. The products of Groups II-LVIII do not share the same or corresponding special technical feature with Group I because they are drawn to products having materially different structures and functions, each defines a separate invention over the art. Therefore, the claims are not linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

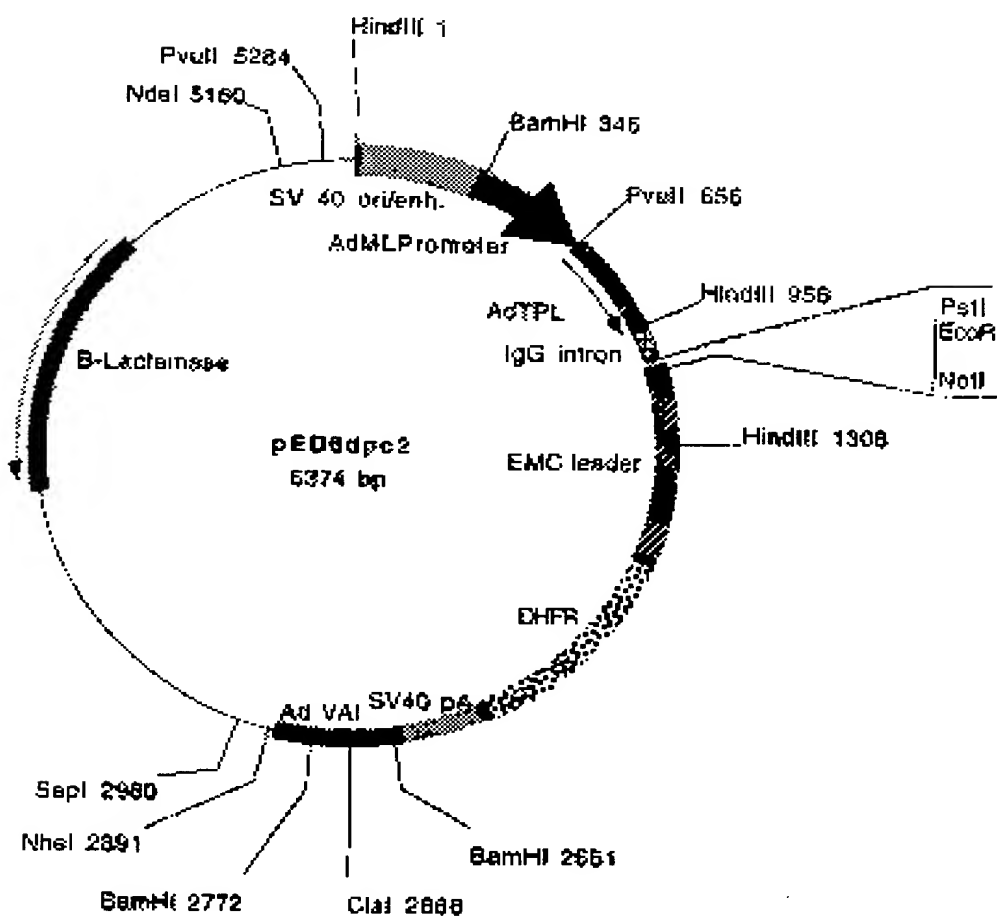
(51) International Patent Classification ⁶ : C07H 21/04, C07K 14/705, C12N 15/09, 15/63, C12Q 1/68		A1	(11) International Publication Number: WO 99/57132
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(21) International Application Number: PCT/US99/09970		(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). McCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LaVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). COLLINS-RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). EVANS, Cheryl; 18801 Bent Willow Circle, Germantown, MD 20874 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 12 Foxrock Court, Dublin 18 (IE). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). STEININGER, Robert, J., II; 100 Reed Street, Cambridge, MA 02140 (US). BOWMAN, Michael, R.; 50 Aldrich Road, Canton, MA 02021 (US). DiBLASIO-SMITH, Elizabeth; 17 Chestnut Road, Tyngsboro, MA 01879 (US). WIDOM, Angela; 19 Cherokee Road, Acton, MA 01720 (US).	
(22) International Filing Date: 7 May 1999 (07.05.99)			
(30) Priority Data:			
60/084,564	7 May 1998 (07.05.98)	US	
60/087,645	2 June 1998 (02.06.98)	US	
60/093,712	22 July 1998 (22.07.98)	US	
60/094,935	31 July 1998 (31.07.98)	US	
60/095,880	10 August 1998 (10.08.98)	US	
60/096,068	11 August 1998 (11.08.98)	US	
09/306,111	6 May 1999 (06.05.99)	US	
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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM			
(57) Abstract			
Novel polynucleotides and the proteins encoded thereby are disclosed.			

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FIGURE 1A

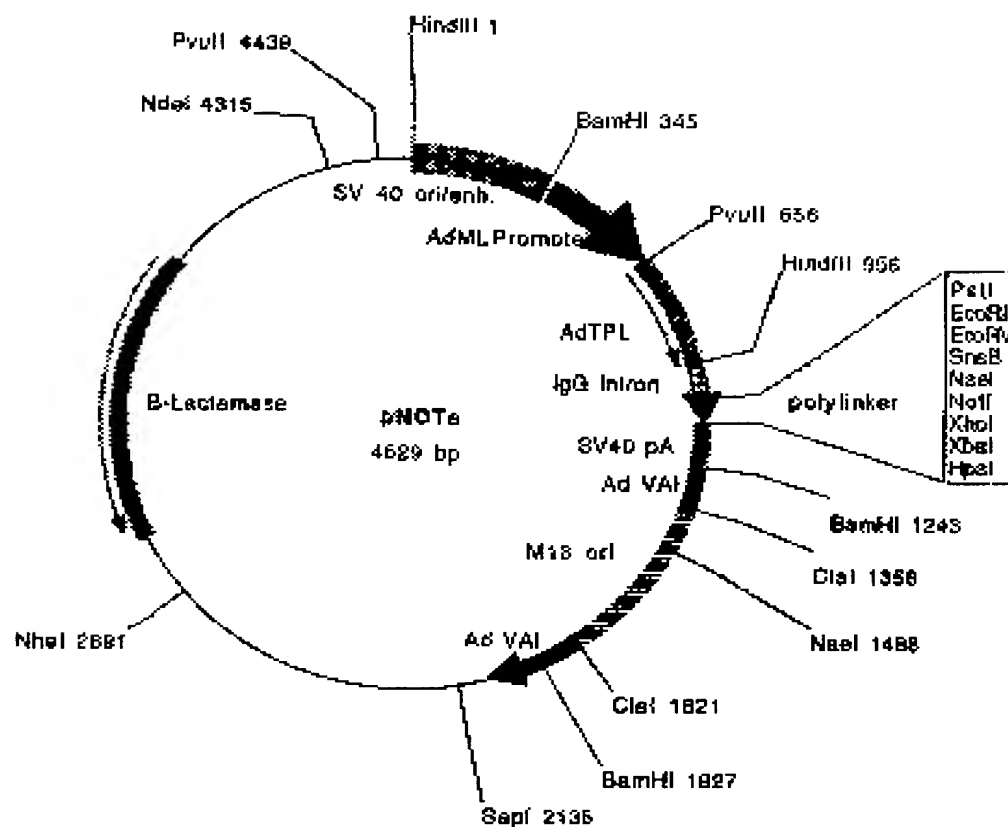


Plasmid name: pED6dpc2

Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al. (1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs
Plasmid size: 4529 bp

Comments/References: pNOTs is a derivative of pMT2 (Kaufman et al, 1988, Mol.Cell.Biol.8:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M18 origin of replication was inserted in the ClaI site. GST cDNAs are cloned between EcoRI and NotI

SEQUENCE LISTING

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 Collins-Racie, Lisa A.
 Evans, Cheryl
 Herberg, David
 Treacy, Maurice
 Agostino, Michael J.
 Steininger II, Robert J.
 Bowman, Michael R.
 DiBlasio-Smith, Elizabeth
 Widom, Angela
 Genetics Institute, Inc.

<120> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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Pro	Pro	His	Pro	Tyr	Lys	Leu	Trp	Lys	Gln	Glu	Arg	Glu	Arg	Arg	Val	
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<212> PRT

<213> Homo sapiens

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Asp Leu His Phe Ile Arg Glu Gly His Arg Tyr Lys Phe Val Asn Ile
 35           40           45

Gln Thr Lys Thr Val Val Val Cys Cys Val Leu Arg Asp Asn Lys Ile
 50           55           60

Leu Pro Met His Phe Pro Leu His Leu Thr Val Pro Lys Phe Ser Leu
 65           70           75           80

Pro Glu His Leu Val Lys Gly Glu Ser Trp Pro Glu Thr Leu Val His
          85           90           95

His Trp Leu Gly Ile Cys Gln Glu Gln Phe Asp Ile Asp Glu Tyr Ser
100           105           110

Arg Ala Val Arg Asp Val Lys Thr Asp Trp Asn Glu Glu Cys Lys Ser
115           120           125

Pro Lys Lys Gly Arg Cys Ser Gly His Asn His Val Pro Asn Ser Leu
130           135           140

Ser Tyr Ala Arg Asp Glu Leu Thr Gln Ser Phe His Arg Leu Ser Val
145           150           155           160

Cys Val Tyr Gly Asn Asn Leu His Gly Asn Ser Glu Val Asn Leu His
165           170           175

Gly Cys Arg Asp Leu Gly Gly Asp Trp Ala Pro Phe Pro His Asp Ile
180           185           190

Leu Pro Tyr Gln Asp Ser Gly Asp Ser Gly Ser Asp Tyr Leu Phe Pro
195           200           205

Glu Ala Ser Glu Glu Ser Ala Gly Ile Pro Gly Lys Ser Glu Leu Pro
210           215           220

Tyr Glu Glu Leu Trp Leu Glu Glu Gly Lys Pro Ser His Gln Pro Leu
225           230           235           240

Thr Arg Ser Leu Ser Glu Lys Asn Arg Cys Asp Gln Phe Arg Gly Ser
245           250           255

Val Arg Ser Lys Cys Ala Thr Ser Pro Leu Pro Ile Pro Gly Thr Leu
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Gly Ala Ala Val Lys Ser Ser Asp Thr Ala Leu Pro Pro Pro Pro Val
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Pro Pro Lys Ser Glu Ala Val Arg Glu Glu Cys Arg Leu Leu Asn Ala

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		450				455					460				
Gly	Cys	Pro	Lys	Ser	Ala	Ser	Tyr	Ser	Leu	Glu	Ser	Thr	Asp	Val	Lys
	465				470					475					480
Ser	Leu	Ala	Ala	Gly	Val	Thr	Lys	Gln	Ser	Thr	Ser	Cys	Pro	Ala	Leu
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Pro	Pro	Arg	Ala	Pro	Lys	Leu	Val	Glu	Glu	Lys	Val	Ala	Ser	Glu	Thr
			500						505					510	
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Gln	Asp	Ile	Phe	Ser	Ala	Ser	Tyr	Pro	Phe	Ser	Ser	Pro	Leu	His	Leu
			545		550					555					560
Gln	Leu	Ala	Pro	Arg	Ser	Cys	Gly	Asp	Gly	Ser	Pro	Trp	Gln	Pro	Pro
			565						570					575	
Ala	Asp	Leu	Ser	Gly	Leu	Ser	Ile	Glu	Glu	Val	Ser	Lys	Ser	Leu	Arg
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Phe	Ile	Gly	Leu	Ser	Glu	Asp	Val	Ile	Ser	Phe	Phe	Val	Thr	Glu	Lys
		595				600							605		
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615

620

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<211> 892

<212> DNA

<213> Homo sapiens

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<311> 155

<312> PRT

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Trp Asn Arg Val Phe Gly His Ser Ser Gly Pro Met Val Glu Lys Tyr
          35          40          45

Ser Val Ala Thr Gln Ile Val Met Gly Gly Val Thr Gly Trp Cys Ala
          50          55          60

Gly Phe Leu Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly
          65          70          75          80

Gly Gly Phe Leu Leu Leu Gln Ile Ala Ser His Ser Gly Tyr Val Gln
          85          90          95

Ile Asp Trp Lys Arg Val Glu Lys Asp Val Asn Lys Ala Lys Arg Gln
          100          105          110

Ile Lys Lys Arg Ala Asn Lys Ala Ala Pro Glu Ile Asn Asn Leu Ile
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Glu Glu Ala Thr Glu Phe Ile Lys Glu Asn Ile Val Ile Ser Ser Gly
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Phe Val Gly Gly Phe Leu Leu Gly Leu Ala Ser
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Ala Cys Thr Cys Leu Leu Asp Pro Ser Thr Trp Arg Pro Ala His Val
35 40 45

Ser Gly Pro Ala Leu Ala Ser Ser Pro Gln Ile Leu Ser Val Phe Ser
 50 55 60
 Leu Gly Phe Pro Gly Phe Val Asn Gly Ser Cys Val Ser Arg Tyr Lys
 65 70 75 80
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 85 90 95
 Ser Val Ser Ile Phe Tyr Leu Gln Leu Leu Cys Ser His Gly His Cys
 100 105 110
 Cys His Thr Glu Ser Gly Pro Leu Leu Ser Phe Ser Asn Trp Pro Pro
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 Trp Lys His His Cys Leu Ala His Ile Leu Thr Tyr Ser Pro Ser Arg
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 <212> DNA
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<210> 12

<211> 126

<212> PRT

<213> Homo sapiens

<400> 12

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Cys Val Leu Gln Val His Ala Ala Lys Val Ile Pro Ala His Pro Cys
                35                      40                      45

Pro Val Ser Val Ser Phe Arg Val Ile Pro Tyr Leu Ser Ile Gly Gly
  50                      55                      60

Leu Ile Leu Leu Asp Phe Leu Lys Thr Leu Arg Trp Ser Ile Arg Ser
  65                      70                      75                      80

Asp Phe Ser His Ser Ser Ala Gly Glu Leu Arg Ile Thr Ser Ser Phe
                85                      90                      95

Gly Arg Trp Ser Trp Val Arg Gly Ser Trp Tyr Thr Val Phe Ile Val
  100                      105                      110

Ser Leu Ile Gln Asn Ala Asn Lys Phe Asn Val Phe Leu Pro
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<210> 13

<211> 1426

<212> DNA

<213> Homo sapiens

<400> 13

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<210> 14

<211> 80

<212> PRT

<213> Homo sapiens

<400> 14

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Met Pro Pro Leu Val Ser Pro Gln Cys Ala Pro Ala His Pro Gly Ser
 1             5             20             15

```

```

Ala Leu Ser Asp Pro Cys Thr Pro Leu Met Ser Pro Arg Arg Ala Ser
 20             25             30

```

```

Cys Ser Ser Pro Ser Ile Tyr Leu Ser Leu Ser Leu Leu Val Gly His
 35             40             45

```

```

Phe Val Cys Arg Ala Val Glu Asn Arg Thr Ser Glu Leu Asn Ile Cys
 50             55             60

```

```

Pro Asp Val Lys Val Leu Phe Met Thr Thr Leu Leu Ser Met Tyr Met
 65             70             75             80

```

<210> 15

<211> 2364

<212> DNA

<213> Homo sapiens

<400> 15

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cctttacaca ggatacaga tctctaaaa cacagttaac taagggtcgc tcaagccctc 660
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```

<210> 15

<211> 463

<212> PRT

<213> Homo sapiens

<400> 16

```

Met Ser Gly Gly Thr Pro Tyr Ile Gly Ser Lys Ile Ser Leu Ile Ser
  1             5             10             15

```

```

Lys Ala Val Ile Arg Tyr Glu Gly Ile Leu Tyr Thr Ile Asp Thr Glu
          20             25             30

```

```

Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp
      35             40             45

```

```

Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr
      50             55             60

```

```

Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro
      65             70             75             80

```

```

Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser
          85             90             95

```

```

Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly
      100             105             110

```

```

Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe Ser Pro Ser Ser Leu
      115             120             125

```

```

Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr
      130             135             140

```

Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr Leu Pro Gln Ser Ser
 145 150 155 160
 Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg Ser Leu Lys Thr Gln
 165 170 175
 Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp Pro Leu Arg Lys Ser
 180 185 190
 Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser Ala His Leu Pro Ala
 195 200 205
 Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser Thr Arg Pro Leu Pro
 210 215 220
 Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu His Arg Gln Ala Glu
 225 230 235 240
 Val His Lys Val Ser Arg Pro Glu Asn Glu Gln Leu Arg Asn Asp Asn
 245 250 255
 Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala Pro Arg Arg Gly Arg
 260 265 270
 Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly Ile Arg Arg Asp Gly
 275 280 285
 Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu Ser Ala Asn Ala Gln
 290 295 300
 Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His Asn Lys Leu Lys Leu
 305 310 315 320
 Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro Val Asn Gly Glu Asp
 325 330 335
 Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser Glu Gly Asn Ala Asp
 340 345 350
 Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr Asp Lys Thr Lys Ser
 355 360 365
 Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg Glu Arg Arg Pro Thr
 370 375 380
 Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr Phe Gly Ile Pro Leu
 385 390 395 400
 Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Leu Gly
 405 410 415
 Phe Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Thr Phe Thr
 420 425 430
 Ala Pro Arg Gly Phe Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Arg
 435 440 445
 Glu Phe Ala Asp Phe Glu Tyr Arg Lys Thr Thr Ala Phe Gly Pro
 450 455 460

<210> 17
 <211> 2760
 <212> DNA
 <213> Homo sapiens

<400> 17
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<210> 18
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Val Leu Ala Leu Ser Gly Ser Asn Val Gly Arg Gln Tyr Leu Ala
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 Gln Gln Leu Thr Leu Leu Gln Asp Leu Phe Ser Leu Leu His Thr Ala
 20 25 30
 Ser Pro Arg Val Gln Arg Gln Val Thr Ser Leu Leu Arg Arg Val Leu
 35 40 45
 Pro Glu Val Thr Pro Ser Arg Leu Ala Ser Ile Ile Gly Val Lys Ser
 50 55 60
 Leu Pro Pro Ala Asp Ile Ser Asp Ile Ile His Ser Thr Glu Lys Gly
 65 70 75 80
 Asp Trp Asn Lys Leu Gly Ile Leu Asp Met Phe Leu Gly Cys Ile Ala
 85 90 95
 Lys Ala Leu Thr Val Gln Leu Lys Ala Lys Gly Thr Thr Ile Thr Gly
 100 105 110
 Thr Ala Gly Thr Thr Val Gly Lys Gly Val Thr Thr Val Thr Leu Pro
 115 120 125
 Met Ile Phe Asn Ser Ser Tyr Leu Arg Arg Gly Glu Ser His Trp Trp
 130 135 140
 Met Lys Gly Ser Thr Pro Thr Gln Ile Ser Glu Ile Ile Ile Lys Leu
 145 150 155 160
 Ile Lys Asp Met Ala Ala Gly His Leu Ser Glu Ala Trp Ser Arg Val
 165 170 175
 Thr Lys Asn Ala Ile Ala Glu Thr Ile Ile Ala Leu Thr Lys Met Glu
 180 185 190
 Glu Glu Phe Arg Ser Pro Val Arg Cys Ile Ala Thr Thr Arg Leu Trp
 195 200 205
 Leu Ala Leu Ala Ser Leu Cys Val Leu Asp Gln Asp His Val Asp Arg
 210 215 220
 Leu Ser Ser Gly Arg Trp Met Gly Lys Asp Gly Gln Gln Lys Gln Met
 225 230 235 240
 Pro Met Cys Asp Asn His Asp Asp Gly Glu Thr Ala Ala Ile Ile Leu
 245 250 255
 Cys Asn Val Cys Gly Asn Leu Cys Thr Asp Cys Asp Arg Phe Leu His
 260 265 270
 Leu His Arg Arg Thr Lys Thr His Gln Arg Gln Val Phe Lys Glu Glu
 275 280 285
 Glu Glu Ala Ile Lys Val Asp Leu His Glu Gly Cys Gly Arg Thr Lys
 290 295 300
 Leu Phe Trp Leu Met Ala Leu Ala Asp Ser Lys Thr Met Lys Ala Met
 305 310 315 320

Val Glu Phe Arg Glu His Thr Gly Lys Pro Thr Thr Ser Ser Ser Glu
 325 330 335
 Ala Cys Arg Phe Cys Gly Ser Arg Ser Gly Thr Glu Leu Ser Ala Val
 340 345 350
 Gly Ser Val Cys Ser Asp Ala Asp Cys Gln Glu Tyr Ala Lys Ile Ala
 355 360 365
 Cys Ser Lys Thr His Pro Cys Gly His Pro Cys Gly Gly Val Lys Asn
 370 375 380
 Glu Glu His Cys Leu Pro Cys Leu His Gly Cys Asp Lys Ser Ala Thr
 385 390 395 400
 Ser Leu Lys Gln Asp Ala Asp Asp Met Cys Met Ile Cys Phe Thr Glu
 405 410 415
 Ala Leu Ser Ala Ala Pro Ala Ile Gln Leu Asp Cys Ser His Ile Phe
 420 425 430
 His Leu Gln Cys Cys Arg Arg Val Leu Glu Asn Arg Trp Leu Gly Pro
 435 440 445
 Arg Ile Thr Phe Gly Phe Ile Ser Cys Pro Ile Cys Lys Asn Lys Ile
 450 455 460
 Asn His Ile Val Leu Lys Asp Leu Leu Asp Pro Ile Lys Glu Leu Tyr
 465 470 475 480
 Glu Asp Val Arg Arg Lys Ala Leu Met Arg Leu Glu Tyr Glu Gly Leu
 485 490 495
 His Lys Ser Glu Ala Ile Thr Thr Pro Gly Val Arg Phe Tyr Asn Asp
 500 505 510
 Pro Ala Gly Tyr Ala Met Asn Arg Tyr Ala Tyr Tyr Val Cys Tyr Lys
 515 520 525
 Cys Arg Lys Ala Tyr Phe Gly Gly Glu Ala Arg Cys Asp Ala Glu Ala
 530 535 540
 Gly Arg Gly Asp Asp Tyr Asp Pro Arg Glu Leu Ile Cys Gly Ala Cys
 545 550 555 560
 Ser Asp Val Ser Arg Ala Gln Met Cys Pro Lys His Gly Thr Asp Phe
 565 570 575
 Leu Glu Tyr Lys Cys Arg Tyr Cys Cys Ser Val Ala Val Phe Phe Cys
 580 585 590
 Phe Gly Thr Thr His Phe Cys Asn Ala Cys His Asp Asp Phe Gln Arg
 595 600 605
 Met Thr Ser Ile Pro Lys Glu Glu Leu Pro His Cys Pro Ala Gly Pro
 610 615 620
 Lys Gly Lys Gln Leu Glu Gly Thr Glu Cys Pro Leu His Val Val His
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Pro Pro Thr Gly Glu Glu Phe Ala Leu Gly Cys Gly Val Cys Arg Asn
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Ala His Thr Phe
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<210> 19
<211> 1649
<212> DNA
<213> Homo sapiens

<400> 19
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<210> 20
<211> 92
<212> PRT
<213> Homo sapiens

<400> 20
Met Gly Glu Pro Ala Gly Gly Glu Asn Pro Pro Leu Ser Pro His Pro
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Pro Gly Arg Ala Asn Val Lys Leu Leu Ile Phe Val Leu Tyr Ile Phe
20 25 30
Tyr Ile Asn Ile Ser Ile Phe Phe Leu Gln Asn Gln Phe Ile Asn Gly
35 40 45
Arg Gly Val Trp Gly Gly His Met Glu Leu Pro Leu Trp Gly Gly Pro
50 55 60

Leu His Tyr Pro Thr Tyr Arg Pro Phe Pro His Pro Pro Pro His Ser
 65 70 75 80

Pro Pro Pro Gly Cys Asp Cys Cys Lys Met Gly Val
 85 90

<210> 21
 <211> 2644
 <212> DNA
 <213> Homo sapiens

<400> 21
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<211> 667
 <212> PRT
 <213> Homo sapiens

<220>
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<400> 22

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      20              25              30

Ser Lys Ala Pro Ala Ser Ser Ser Ser Asn Pro Glu Glu Val Gln Lys
      35              40              45

Glu Gly Pro Thr Ala Leu Gln Asp Ser Asn Ser Gly Glu Pro Asp Ile
 50              55              60

Pro Pro Pro Gln Pro Asp Cys Gly Asp Phe Arg Ser Leu Gln Glu Glu
 65              70              75              80

Gln Ser Arg Pro Thr Thr Ala Val Ser Ser Pro Gly Gly Pro Ala Arg
      85              90              95

Ala Pro Pro Tyr Gln Glu Pro Pro Trp Gly Gly Pro Ala Thr Ala Pro
    100              105              110

Tyr Ser Leu Glu Thr Leu Lys Gly Gly Thr Ile Leu Gly Thr Arg Ser
    115              120              125

Leu Lys Gly Thr Ser Tyr Cys Leu Phe Gly Arg Leu Ser Gly Cys Asp
    130              135              140

Val Cys Leu Glu His Pro Ser Val Ser Arg Tyr His Ala Val Leu Gln
    145              150              155              160

His Arg Ala Ser Gly Pro Asp Gly Glu Cys Asp Ser Asn Gly Pro Gly
    165              170              175

Phe Tyr Leu Tyr Asp Leu Gly Ser Thr His Gly Thr Phe Leu Asn Lys
    180              185              190

Thr Arg Ile Pro Pro Arg Thr Tyr Cys Arg Val His Val Gly His Val
    195              200              205

Val Arg Phe Gly Gly Ser Thr Arg Leu Phe Ile Leu Gln Gly Pro Glu
    210              215              220

Glu Asp Arg Glu Ala Glu Ser Glu Leu Thr Val Thr Gln Leu Lys Glu
    225              230              235              240

Leu Arg Lys Gln Gln Gln Ile Leu Leu Xaa Lys Lys Met Leu Gly Glu
    245              250              255

Asp Ser Asp Glu Glu Glu Glu Met Asp Thr Ser Glu Arg Lys Ile Asn
    260              265              270
  
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 305 310 315 320
 Gln Gly Phe Phe Asp Arg Glu Gly Glu Glu Leu Glu Tyr Glu Phe Asp
 325 330 335
 Glu Gln Gly His Ser Thr Trp Leu Cys Arg Val Arg Leu Pro Val Asp
 340 345 350
 Asp Ser Thr Gly Lys Gln Leu Val Ala Glu Ala Ile His Ser Gly Lys
 355 360 365
 Lys Lys Glu Ala Met Ile Gln Cys Ser Leu Glu Ala Cys Arg Ile Leu
 370 375 380
 Asp Thr Leu Gly Leu Leu Arg Gln Glu Ala Val Ser Arg Lys Arg Lys
 385 390 395 400
 Ala Lys Asn Trp Glu Asp Glu Asp Phe Tyr Asp Ser Asp Asp Asp Thr
 405 410 415
 Phe Leu Asp Arg Thr Gly Leu Ile Glu Lys Lys Arg Leu Asn Arg Met
 420 425 430
 Lys Lys Ala Gly Lys Ile Asp Glu Lys Pro Glu Thr Phe Glu Ser Leu
 435 440 445
 Val Ala Lys Leu Asn Asp Ala Glu Arg Glu Leu Ser Glu Ile Ser Glu
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 Arg Leu Lys Ala Ser Ser Gln Val Leu Ser Glu Ser Pro Ser Gln Asp
 465 470 475 480
 Ser Leu Asp Ala Phe Met Ser Glu Met Lys Ser Gly Ser Thr Leu Asp
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 Gly Val Ser Arg Lys Lys Leu His Leu Arg Thr Phe Glu Leu Arg Lys
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 Glu Gln Gln Arg Leu Lys Gly Leu Ile Lys Ile Val Lys Pro Ala Glu
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 Ile Pro Glu Leu Lys Lys Thr Glu Thr Gln Thr Thr Gly Ala Glu Asn
 530 535 540
 Lys Ala Lys Lys Leu Thr Leu Pro Leu Phe Gly Ala Met Lys Gly Gly
 545 550 555 560
 Ser Lys Phe Lys Leu Lys Thr Gly Thr Val Gly Lys Leu Pro Pro Lys
 565 570 575
 Arg Pro Glu Leu Pro Pro Thr Leu Met Arg Met Lys Asp Glu Pro Glu
 580 585 590

Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Lys Glu
 595 600 605

Glu His Glu Lys Lys Lys Leu Glu Asp Gly Ser Leu Ser Arg Pro Gln
 610 615 620

Pro Glu Ile Glu Pro Glu Ala Ala Val Gln Glu Met Arg Pro Pro Thr
 625 630 635 640

Asp Leu Thr His Phe Lys Glu Thr Gln Thr His Gly Asn Ile Phe Leu
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Leu Leu Pro Val Leu Phe Ser Gly Gln Leu His
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<210> 23

<211> 2402

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24

<211> 520

<212> PRT

<213> Homo sapiens

<400> 24

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          20              25              30

Ala Ser Gly Val Ser Val Ala Ser Ala Ala Leu Ala Ala Ser Ala Ala
          35              40              45

Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser Gly Phe Ala Pro
          50              55              60

Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp Tyr Asn Gly Leu Pro
          65              70              75              80

Val Leu Thr Thr Asn Ala Ile Gly Gln Trp Asp Leu Val Cys Asp Leu
          85              90              95

Gly Trp Gln Val Ile Leu Glu Gln Ile Leu Phe Ile Leu Gly Phe Ala
          100              105              110

Ser Gly Tyr Leu Phe Leu Gly Tyr Pro Ala Asp Arg Phe Gly Arg Arg
          115              120              125

Gly Ile Val Leu Leu Thr Leu Gly Leu Val Gly Pro Cys Gly Val Gly
          130              135              140

Gly Ala Ala Ala Gly Ser Ser Thr Gly Val Met Ala Leu Arg Phe Leu
          145              150              155              160

Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg
          165              170              175

Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly
          180              185              190

Glu Leu Val Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu
          195              200              205

Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys
          210              215              220

Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala
          225              230              235              240

Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu
          245              250              255

Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu
          260              265              270

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Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro
 275 280 285
 Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu Leu Asn Tyr Arg Asn Ile
 290 295 300
 Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr Asn Phe Ile Ala His Ala
 305 310 315 320
 Ile Arg His Cys Tyr Gln Pro Val Gly Gly Gly Gly Ser Pro Ser Asp
 325 330 335
 Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly Thr Ala Ala Leu Ala Cys
 340 345 350
 Val Phe Leu Gly Val Thr Val Asp Arg Phe Gly Arg Arg Gly Ile Leu
 355 360 365
 Leu Leu Ser Met Thr Leu Thr Gly Ile Ala Ser Leu Val Leu Leu Gly
 370 375 380
 Leu Trp Asp Tyr Leu Asn Glu Ala Ala Ile Thr Thr Phe Ser Val Leu
 385 390 395 400
 Gly Leu Phe Ser Ser Gln Ala Ala Ala Ile Leu Ser Thr Leu Leu Ala
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 Ala Glu Val Ile Pro Thr Thr Val Arg Gly Arg Gly Leu Gly Leu Ile
 420 425 430
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 435 440 445
 His Met Gly His Gly Ala Phe Leu Gln His Val Val Leu Ala Ala Cys
 450 455 460
 Ala Leu Leu Cys Ile Leu Ser Ile Met Leu Leu Pro Glu Thr Lys Arg
 465 470 475 480
 Lys Leu Leu Pro Glu Val Leu Arg Asp Gly Glu Leu Cys Arg Arg Pro
 485 490 495
 Ser Leu Leu Arg Gln Pro Pro Pro Thr Arg Cys Asp His Val Pro Leu
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 Leu Ala Thr Pro Asn Pro Ala Leu
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<210> 25
 <211> 2377
 <212> DNA
 <213> Homo sapiens

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<210> 26

<211> 351

<212> PRT

<213> Homo sapiens

<400> 26

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```

```

Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr
  20              25              30

```

```

Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu
  35              40              45

```

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Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu
  50              55              60

```

```

Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys
  65              70              75              80

```

```

Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val
  85              90              95

```

Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu
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 Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu
 115 120 125
 Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His
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 Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro
 145 150 155 160
 Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys
 165 170 175
 Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly
 180 185 190
 His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe
 195 200 205
 Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val
 210 215 220
 Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys
 225 230 235 240
 Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln
 245 250 255
 Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr
 260 265 270
 Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg
 275 280 285
 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe
 290 295 300
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp
 305 310 315 320
 Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn
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<210> 27

<211> 460

<212> DNA

<213> Homo sapiens

<400> 27

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aaaaaaaaaa aaaaaaanaa aaaaaaanaa aaaaaaanaa 460

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<210> 28
 <211> 85
 <212> PRT
 <213> Homo sapiens

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<400> 28
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          20             25             30
Ala Ala Asp Glu Lys Pro Phe Met Gln Thr Phe Leu Thr Ile Leu Lys
          35             40             45
Ile Phe Leu Met Met Met Thr Ser Ser Glu Met Pro Ser Gly Cys Arg
          50             55             60
Arg Gly Gln Ala Leu Gly Thr Glu Pro Gln Cys Glu Pro Ala Gln Asp
          65             70             75             80
Ser Phe Arg Trp Phe
                      85

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<210> 29
 <211> 3204
 <212> DNA
 <213> Homo sapiens

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<400> 29
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<210> 30

<211> 741

<212> PAT

<213> Homo sapiens

<400> 30

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Met Ala Glu Pro Val Ser Pro Leu Lys His Phe Val Leu Ala Lys Lys
  1             5             10             15

```

```

Ala Ile Thr Ala Ile Phe Asp Gln Leu Leu Glu Phe Val Thr Glu Gly
      20             25             30

```

```

Ser His Phe Val Glu Ala Thr Tyr Lys Asn Pro Glu Leu Asp Arg Ile
      35             40             45

```

```

Ala Thr Glu Asp Asp Leu Val Glu Met Gln Gly Tyr Lys Asp Lys Leu
      50             55             60

```

```

Ser Ile Ile Gly Glu Val Leu Ser Arg Arg His Met Lys Val Ala Phe
      65             70             75             80

```

```

Phe Gly Arg Thr Ser Ser Gly Lys Ser Ser Val Ile Asn Ala Met Leu
      85             90             95

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```

Tyr Asp Lys Val Leu Pro Ser Gly Ile Gly His Ile Thr Asn Cys Phe
     100             105             110

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Leu Ser Val Glu Gly Thr Asp Gly Asp Lys Ala Tyr Leu Met Thr Glu
     115             120             125

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Gly Ser Asp Glu Lys Lys Ser Val Lys Thr Val Asn Gln Leu Ala His
 130 135 140
 Ala Leu His Met Asp Lys Asp Leu Lys Ala Gly Cys Leu Val Arg Val
 145 150 155 160
 Phe Trp Pro Lys Ala Lys Cys Ala Leu Leu Arg Asp Asp Leu Val Leu
 165 170 175
 Val Asp Ser Pro Gly Thr Asp Val Thr Thr Glu Leu Asp Ser Trp Ile
 180 185 190
 Asp Lys Phe Cys Leu Asp Ala Asp Val Phe Val Leu Val Ala Asn Ser
 195 200 205
 Glu Ser Thr Leu Met Asn Thr Glu Lys His Phe Phe His Lys Val Asn
 210 215 220
 Glu Arg Leu Ser Lys Pro Asn Ile Phe Ile Leu Asn Asn Arg Trp Asp
 225 230 235 240
 Ala Ser Ala Ser Glu Pro Glu Tyr Met Glu Asp Val Arg Arg Gln His
 245 250 255
 Met Glu Arg Cys Leu His Phe Leu Val Glu Glu Leu Lys Val Val Asn
 260 265 270
 Ala Leu Glu Ala Gln Asn Arg Ile Phe Phe Val Ser Ala Lys Glu Val
 275 280 285
 Leu Ser Ala Arg Lys Gln Lys Ala Gln Gly Met Pro Glu Ser Gly Val
 290 295 300
 Ala Leu Ala Glu Gly Phe His Ala Arg Leu Gln Glu Phe Gln Asn Phe
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 Glu Gln Ile Phe Glu Glu Cys Ile Ser Gln Ser Ala Val Lys Thr Lys
 325 330 335
 Phe Glu Gln His Thr Ile Arg Ala Lys Gln Ile Leu Ala Thr Val Lys
 340 345 350
 Asn Ile Met Asp Ser Val Asn Leu Ala Ala Glu Asp Lys Arg His Tyr
 355 360 365
 Ser Val Glu Glu Arg Glu Asp Gln Ile Asp Arg Leu Asp Phe Ile Arg
 370 375 380
 Asn Gln Met Asn Leu Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu
 385 390 395 400
 Val Thr Glu Glu Val Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu
 405 410 415
 Ile Cys Arg Leu Ser Val Leu Val Asp Glu Phe Cys Ser Glu Phe His
 420 425 430
 Pro Asn Pro Asp Val Leu Lys Ile Tyr Lys Ser Glu Leu Asn Lys His
 435 440 445

Ile Glu Asp Gly Met Gly Arg Asn Leu Ala Asp Arg Cys Thr Asp Glu
 450 455 460
 Val Asn Ala Leu Val Pro Gln Thr Gln Gln Glu Ile Ile Glu Asn Leu
 465 470 475 480
 Lys Pro Leu Leu Pro Ala Gly Ile Gln Asp Lys Leu His Thr Leu Ile
 485 490 495
 Pro Cys Lys Lys Phe Asp Leu Ser Tyr Asn Leu Asn Tyr His Lys Leu
 500 505 510
 Cys Ser Asp Phe Gln Glu Asp Ile Val Phe Arg Phe Ser Leu Gly Trp
 515 520 525
 Ser Ser Leu Val His Arg Phe Leu Gly Pro Arg Asn Ala Gln Arg Val
 530 535 540
 Leu Leu Gly Leu Ser Glu Pro Ile Phe Gln Leu Pro Arg Ser Leu Ala
 545 550 555 560
 Ser Thr Pro Thr Ala Pro Thr Thr Pro Ala Thr Pro Asp Asn Ala Ser
 565 570 575
 Gln Glu Gln Leu Met Ile Thr Leu Val Thr Gly Leu Ala Ser Val Thr
 580 585 590
 Ser Arg Thr Ser Met Gly Ile Ile Ile Val Gly Gly Val Ile Trp Lys
 595 600 605
 Thr Ile Gly Trp Lys Leu Leu Ser Val Ser Leu Thr Met Tyr Gly Ala
 610 615 620
 Leu Tyr Leu Tyr Glu Arg Leu Ser Trp Thr Thr His Ala Lys Glu Arg
 625 630 635 640
 Ala Phe Lys Gln Gln Phe Val Asn Tyr Ala Thr Glu Lys Leu Arg Met
 645 650 655
 Ile Val Ser Ser Thr Ser Ala Asn Cys Ser His Gln Val Lys Gln Gln
 660 665 670
 Ile Ala Thr Thr Phe Ala Arg Leu Cys Gln Gln Val Asp Ile Thr Gln
 675 680 685
 Lys Gln Leu Glu Glu Glu Ile Ala Arg Leu Pro Lys Glu Ile Asp Gln
 690 695 700
 Leu Glu Lys Ile Gln Asn Asn Ser Lys Leu Leu Arg Asn Lys Ala Val
 705 710 715 720
 Gln Leu Glu Asn Glu Leu Glu Asn Phe Thr Lys Gln Phe Leu Pro Ser
 725 730 735
 Ser Asn Glu Asp Ser
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<210> 31

<211> 2483
 <212> DNA
 <213> Homo sapiens

<400> 31

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<210> 32
 <211> 654
 <212> PRK
 <213> Homo sapiens

<400> 32

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                20                      25                      30

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 Ala Ala Pro Val Pro Gly Val Ala Gln Gln Gly Val Ser Leu Gln Pro
 50 55 60
 Gly Thr Thr Gln Ile Cys Thr Gln Thr Asp Pro Phe Gln Gln Thr Phe
 65 70 75 80
 Ile Val Cys Pro Pro Ala Phe Gln Thr Gly Leu Gln Ala Thr Thr Lys
 85 90 95
 His Ser Gly Phe Pro Val Arg Met Asp Asn Ala Val Pro Ile Val Pro
 100 105 110
 Gln Ala Pro Ala Ala Gln Pro Thr Thr Asp Ser Val Arg Ser Ser His
 115 120 125
 Ala Asp Leu Gln Gly Lys Asn Ile Gln Thr Phe Leu Arg Asn Gly Leu
 130 135 140
 Leu Arg Lys Leu Tyr Thr Thr Asn Gly Ser Asn Ser Pro Pro Ser Ser
 145 150 155 160
 Ser His Ile Thr Pro Gln Tyr Ala Val Pro Phe Thr Leu Ser Cys Ala
 165 170 175
 Ala Gly Arg Pro Ala Leu Val Gln Gln Thr Ala Ala Val Leu Gln Ala
 180 185 190
 Trp Pro Gly Gly Thr Gln Gln Ile Leu Leu Pro Ser Thr Trp Gln Gln
 195 200 205
 Leu Pro Gly Val Ala Leu His Asn Ser Val Gln Pro Thr Ala Met Ile
 210 215 220
 Pro Gln Ala Met Gly Ser Gly Gln Gln Leu Ala Asp Trp Arg Asn Ala
 225 230 235 240
 His Ser His Gly Asn Gln Tyr Ser Thr Ile Met Gln Gln Pro Ser Leu
 245 250 255
 Leu Thr Asn His Val Thr Leu Ala Thr Ala Gln Pro Leu Asn Val Gly
 260 265 270
 Val Ala His Val Val Arg Gln Gln Gln Ser Ser Ser Leu Pro Ser Lys
 275 280 285
 Lys Asn Lys Gln Ser Ala Pro Val Ser Ser Lys Ser Ser Leu Asp Val
 290 295 300
 Leu Pro Ser Gln Val Tyr Ser Leu Val Gly Ser Ser Pro Leu Arg Thr
 305 310 315 320
 Thr Ser Ser Tyr Asn Ser Leu Val Pro Val Gln Asp Gln His Gln Pro
 325 330 335
 Ile Ile Ile Pro Asp Thr Pro Ser Pro Pro Val Ser Val Ile Thr Ile
 340 345 350

Arg Ser Asp Thr Asp Glu Glu Glu Asp Asn Lys Tyr Lys Pro Ser Ser
 355 360 365
 Ser Gly Leu Lys Pro Arg Ser Asn Val Ile Ser Tyr Val Thr Val Asn
 370 375 380
 Asp Ser Pro Asp Ser Asp Ser Ser Leu Ser Ser Pro Tyr Ser Thr Asp
 385 390 395 400
 Thr Leu Ser Ala Leu Arg Gly Asn Ser Gly Ser Val Leu Glu Gly Pro
 405 410 415
 Gly Arg Val Val Ala Asp Gly Thr Gly Thr Arg Thr Ile Ile Val Pro
 420 425 430
 Pro Leu Lys Thr Gln Leu Gly Asp Cys Thr Val Ala Thr Gln Ala Ser
 435 440 445
 Gly Leu Leu Ser Asn Lys Thr Lys Pro Val Ala Ser Val Ser Gly Gln
 450 455 460
 Ser Ser Gly Cys Cys Ile Thr Pro Thr Gly Tyr Arg Ala Gln Arg Gly
 465 470 475 480
 Gly Thr Ser Ala Ala Gln Pro Leu Asn Leu Ser Gln Asn Gln Gln Ser
 485 490 495
 Ser Ala Ala Pro Thr Ser Gln Glu Arg Ser Ser Asn Pro Ala Pro Arg
 500 505 510
 Arg Gln Gln Ala Phe Val Ala Pro Leu Ser Gln Ala Pro Tyr Thr Phe
 515 520 525
 Gln His Gly Ser Pro Leu His Ser Thr Gly His Pro His Leu Ala Pro
 530 535 540
 Ala Pro Ala His Leu Pro Ser Gln Ala His Leu Tyr Thr Tyr Ala Ala
 545 550 555 560
 Pro Thr Ser Ala Ala Ala Leu Gly Ser Thr Ser Ser Ile Ala His Leu
 565 570 575
 Phe Ser Pro Gln Gly Ser Ser Arg His Ala Ala Ala Tyr Thr Thr His
 580 585 590
 Pro Ser Thr Leu Val His Gln Val Pro Val Ser Val Gly Pro Ser Leu
 595 600 605
 Leu Thr Ser Ala Ser Val Ala Pro Ala Gln Tyr Gln His Gln Phe Ala
 610 615 620
 Thr Gln Ser Tyr Ile Gly Ser Ser Arg Gly Ser Thr Ile Tyr Thr Gly
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<210> 33

<211> 2731

<212> DNA
<213> Homo sapiens

<220>

<221> Feature

<222> (2173)

<220>

<221> Feature

<222> (2700)

<400> 30

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<210> 34

<211> 441

<212> PRT

<213> Homo sapiens

<400> 34

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Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
          20              25              30

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
          35              40              45

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
  50              55              60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
  65              70              75              80

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
          85              90              95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
          100              105              110

Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys
          115              120              125

Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg
          130              135              140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn
          145              150              155              160

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr
          165              170              175

Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser
          180              185              190

Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met
          195              200              205

Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr
          210              215              220

Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe
          225              230              235              240

Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu
          245              250              255

Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu
          260              265              270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg His Lys Gly Glu
          275              280              285

Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys

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290 295 300

Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly
305 310 315 320

Ile Val Lys Pro Arg Leu Gly Val Thr Leu His Lys Val Val Val Ala
325 330 335

Gly Ala Leu Tyr Leu Leu Phe Ser Gly Met Glu Gly Val Leu Arg Val
340 345 350

Thr Gly Ala Gln Thr Asp Leu Ala Ser Leu Ala Phe Ile Pro Leu Ala
355 360 365

Phe Leu Asp Thr Ala Leu Cys Trp Trp Ile Phe Ile Ser Leu Thr Gln
370 375 380

Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu
385 390 395 400

Tyr Arg His Phe Thr Asn Thr Leu Ile Leu Ala Val Ala Ala Ser Ile
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Val Phe Ile Ile Trp Thr Thr Met Lys Phe Arg Ile Val Thr Cys Gln
420 425 430

Ser Val Ser Tyr Lys His Ile Tyr Glu
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<210> 35

<221> 1670

<212> DNA

<213> Homo sapiens

<400> 35

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```

tcagaaatgtg tctctctcat ctaatgctca tctgtttaat gctgatgect cgcgtacagg 1500
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```

<210> 36
 <211> 164
 <212> PRT
 <213> Homo sapiens

```

<400> 36
Met Gly Gly Met Val Arg Glu Glu Ala Leu Ala Trp Met Cys Arg Glu
  1                      5                      10                      15

Pro Arg Lys Ala Phe Ser Ala Ile Val Gly Pro Ser Leu Gly Pro Asp
      20                      25                      30

Ser Thr Pro Gly Trp Gly Thr Gly Glu Trp Ala Thr Gly Gly Ala Ile
      35                      40                      45

Leu Gly Arg Pro Thr Pro Cys Ala Val Pro Gly Thr Gly Phe Ser Leu
      50                      55                      60

Leu Ser Thr Cys Ser Ser Pro Arg Gly Pro Val Pro Glu Thr Gly Arg
      65                      70                      75                      80

Gly Trp Arg Val Pro Thr Pro Cys Ser Leu Pro Asp Leu Leu Arg Asp
      85                      90                      95

Asp Asp Ala Val Cys Val Pro His Val Gly Pro Pro Pro Ala Cys His
      100                      105                      110

Leu Asn Ala Leu His Gly Pro Val Cys Gly Thr Gly Gly Gln Val Gln
      115                      120                      125

Trp Cys Ala Glu Leu His Trp Glu Asp Phe Gln Arg Gly Arg Ala Ala
      130                      135                      140

Gly Ile Leu Arg Trp Ile Asn Pro Ser Pro Pro Gly Arg Cys Gly Phe
      145                      150                      155                      160

Leu Val Gly Leu

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<210> 37
 <211> 1493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (1415)

```

<400> 37
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gacgggcagc cggcaagatg cgcgcgcctt gccgcgcctg tctcactt tctggcgtt 180
catgatcttg gccagctctg tcatgcctt ctcagctcag ctggccgcgc gcacctgtga 240
gattgtgacc ttggacgggg acagcagcca gactcgagg acgatgcgc gccagaccgc 300

```

```

ccgctgtgac tctagaaagg ggcagatcgc cggcaccacg agagcccgcc cccctctgtg 360
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aggtcgagac ttgttaatac accggtccag ctggacgtgc acccagcccg ggcggaggt 480
aaagaccacc acggtctcct gacaaacaca gcccctgagg ggcgccggga gtggccttgg 540
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tctgcggccc gcccaatccg ttctccctgt gtccgtgaaq gacggcctca ggccttgga 660
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ctgcccatac gatacccat ttagctcag aaganaaaga aaactcaggt aacacttgtt 1440
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```

<210> 38

<211> 132

<212> PRT

<213> Homo sapiens

<400> 38

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Met Ala Pro Ser Pro Arg Thr Gly Ser Arg Gln Asp Ala Thr Ala Leu
  1             5             10             15

```

```

Pro Ser Met Ser Ser Thr Phe Trp Ala Phe Met Ile Leu Ala Ser Leu
          20             25             30

```

```

Leu Ile Ala Tyr Cys Ser Gln Leu Ala Ala Gly Thr Cys Glu Ile Val
      35             40             45

```

```

Thr Leu Asp Arg Asp Ser Ser Gln Pro Arg Arg Thr Ile Ala Arg Gln
      50             55             60

```

```

Thr Ala Arg Cys Ala Cys Arg Lys Gly Gln Ile Ala Gly Thr Thr Arg
      65             70             75             80

```

```

Ala Arg Pro Ala Cys Val Asp Ala Arg Ile Ile Lys Thr Lys Gln Trp
          85             90             95

```

```

Cys Asp Met Leu Pro Cys Leu Glu Gly Glu Gly Cys Asp Leu Leu Ile
      100             105             110

```

```

Asn Arg Ser Gly Trp Thr Cys Thr Gln Pro Gly Gly Arg Ile Lys Thr
      115             120             125

```

```

Thr Thr Val Ser
      130

```

<210> 39

<211> 3693

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (108)

<400> 39

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gatactttag ttctcgaaat cccgtctctt gctttctaga ctttcactac ttccactgac 600
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3693

<210> 40

<211> 230

<212> PRT

<213> Homo sapiens

<400> 40

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Met Leu Arg Phe Val Gln Lys Arg Gly Asn Ser Thr Val Tyr Glu Trp
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Arg Thr Gly Thr Glu Pro Ser Val Val Glu Arg Pro His Leu Glu Glu
      20             25             30

Leu Pro Glu Gln Val Ala Glu Asp Ala Ile Asp Trp Gly Asp Phe Gly
      35             40             45

Val Glu Ala Val Ser Glu Gly Thr Asp Ser Gly Ile Ser Ala Glu Ala
      50             55             60

Ala Gly Ile Asp Trp Gly Ile Phe Pro Glu Ser Asp Ser Lys Asp Pro
      65             70             75             80

Gly Gly Asp Gly Ile Asp Trp Gly Asp Asp Ala Val Ala Leu Gln Ile
      85             90             95

Thr Val Leu Glu Ala Gly Thr Gln Ala Pro Glu Gly Val Ala Arg Gly
     100             105             110

Pro Asp Ala Leu Thr Leu Leu Glu Tyr Thr Glu Thr Arg Asn Gln Phe
     115             120             125

Leu Asp Glu Leu Met Glu Leu Glu Ile Phe Leu Ala Gln Arg Ala Val
     130             135             140

Glu Leu Ser Glu Glu Ala Asp Val Leu Ser Val Ser Gln Phe Gln Leu
     145             150             155             160

Ala Pro Ala Ile Leu Gln Gly Gln Thr Lys Glu Lys Met Val Thr Met
     165             170             175

Val Ser Val Leu Glu Asp Leu Ile Gly Lys Leu Thr Ser Leu Gln Leu
     180             185             190

Gln His Leu Phe Met Ile Leu Ala Ser Pro Arg Ser Gly Phe Pro Leu
     195             200             205

Met Gln Gly Ser Ala Ile Leu Ser Ser Ser Ala Ser Leu Tyr Ser Ser
     210             215             220

Ser Cys Ser Met Thr Pro
     225             230

```

<210> 41
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<400> 41
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 aaggccctcc agcatctggg actcgagagt ggttagcccc tctacctctt ggagctgac 180
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 aaaaaaaa aaaaaaaa a a 1701

<210> 42
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Lys Asp Val Gly Pro Glu Ser Cys Gly Gln Pro Thr Pro Cys Trp
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 Pro Ser Pro Ala Leu Glu Ser Val Leu Gly Lys Ala Ser Gln His Leu
 20 25 30
 Gly Leu Glu Ser Gly Gln Pro Leu Tyr Leu Leu Glu Leu Asn Trp Gly
 35 40 45
 Gly Thr Glu Cys Val Leu Ser Ser Thr Gly Arg Thr Ala Ala Cys Phe
 50 55 60
 Leu Pro Thr Ser Leu Leu Pro Thr Ser Pro Ala Ala Trp Leu Gly Pro
 65 70 75 80
 Glu Ala Leu Cys Leu Pro Gly Arg Pro Gly Thr Thr Gly Leu Arg Asp
 85 90 95

Thr Gly Gly Pro Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Thr
 100 105 110
 Thr Arg Trp Cys Trp Met Leu Val Leu Trp Pro Ala Lys Val His Gly
 115 120 125
 Asp Ser Pro His Gly Ile Leu Arg Asp Gln Ala Ala Gly Ile Gly Lys
 130 135 140
 Glu Phe His Pro Asp Arg Cys Pro Ser Gln Val Pro Arg Arg Pro His
 145 150 155 160
 His Thr Pro Phe Gln Gly Gln Gly Ser Ser Lys Pro Arg Ala Arg Ile
 165 170 175
 Leu Cys Cys Cys Leu Val Glu Ser Leu Pro Pro Cys Val Gly Ser Val
 180 185 190
 Gly Gln Ala Glu Cys Ile Gly Asp Arg Ala Val Ser Met Gly Leu Gly
 195 200 205
 Val Cys Glu Leu Arg Pro Arg Cys Ala Val Trp Arg Arg Val Leu Ser
 210 215 220
 Gly Lys Arg Cys Gly Phe Lys Val Cys Val Cys Arg Gly Trp Val Cys
 225 230 235 240

<210> 43

<211> 1784

<212> DNA

<213> Homo sapiens

<400> 43

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ttaagtacag tgataaagca tatatatctt gtaaaaaaaa aaaaatctg cttatgcatg 240
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cttgacatat actggaaatg catgtatact ggcgtacttt atattctcta aaatgcttaa 360
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```



```

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aaaaaaanaa aaaaaanaa aaaaaaanaa aaaaaaanaa aaaa 1784

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<210> 44
 <211> 82
 <212> PRT
 <213> Homo sapiens

```

<400> 44
Met Cys His Lys Ile Cys Thr Phe Phe Thr Phe Phe Pro Leu Tyr Ile
  1             5             10             15

Ser Tyr Gly Leu Gln Leu Val His Ser Glu Asn Asn Asn Asn Lys Ser
          20             25             30

Pro Phe Ile Phe Phe Asn Asn Cys Ile Ser Ala Gln Val Ile His Tyr
          35             40             45

Ser Leu Lys Pro Cys Leu Cys Asn Leu Thr Ser Asp Met Leu Ala Ile
          50             55             60

Lys Ala Cys Thr Cys Asn Asn Glu Lys Glu Lys Ala Phe Tyr Ile Thr
          65             70             75             80

Thr Gln

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<210> 45
 <211> 1034
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (598)

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<400> 45
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<210> 46

<211> 126
 <212> PRT
 <213> Homo sapiens

<400> 46

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Met Ala Ala Ser Gly Ala Glu Pro Gln Val Leu Val Gln Tyr Leu Val
  1             5             10             15

Leu Arg Lys Asp Leu Ser Gln Ala Pro Phe Ser Trp Pro Ala Gly Ala
      20             25             30

Leu Val Ala Gln Ala Cys His Ala Ala Thr Ala Ala Leu His Thr His
      35             40             45

Arg Asp His Pro His Thr Ala Ala Tyr Leu Gln Glu Leu Gly Arg Met
      50             55             60

Arg Lys Val Val Leu Glu Ala Pro Asp Glu Thr Thr Leu Lys Glu Leu
      65             70             75             80

Ala Glu Thr Leu Gln Gln Lys Asn Ile Asp His Met Leu Trp Leu Glu
      85             90             95

Gln Pro Glu Asn Ile Ala Thr Cys Ile Ala Leu Arg Pro Tyr Pro Lys
      100            105            110

Glu Glu Val Gly Gln Tyr Leu Lys Lys Phe Arg Leu Phe Lys
      115            120            125
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<210> 47
 <211> 1626
 <212> DNA
 <213> Homo sapiens

<400> 47

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ggaggagcaa aaatcagtgga actttttacag aagaacotgc cagcctgtga tgatcctacc 180
aaagagaaac ctcaatlgagc tatggaaatt ccttttttgt gaatttgagt ctgttttttgc 240
ttttctcaga ttccaaatga gagtataca tttcttttgt ttgatgtgct ggttgagatc 300
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tttattttat ccgagaatag agaccatktc gatgatgtat acagggaaca acctaaactc 420
tgctgagcca ctgtttgaac aaataaactc acttaatgtt aatttcaaca cacaaagaa 480
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cttcgttaag attttgttga atgaagaaga tatgaatgta attgtatag actggaagcc 600
gggtgctaca acttttattt alaatagaga agttaaaac actagaanaa ttgctgtgag 660
tttgagtgtg caccatana atcttttgaa gcatggtgca tctcttgaca attttcattt 720
cataggtgtg agtttagggg ctcatatcag tggatttgtt ggaagatat ttcattgtoa 780
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aattcaattc attaatgca accaccagag agcagttcac ttgttcattg catctttaga 960
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atgtgtggac tgtgactgtt ttaaggaana atcatgtcct cggctgggtt atcaagccaa 1080
gctattttaa ggtgttttaa aagaaggat ggaaggaga cctcttagga ccatgtgtgt 1140
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aaaagttcta agcgtatcag gagaaggaga cctcctggc taactgtgtg aaacctgtc 1380
tctaataaaa atkcaaaaa ttagctgggc atggtggcac gtgctgtag tccagctac 1440
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tcaggagagct gaggaagag gatgcttga acccaggagg tggaggttgc agtgagctga 1500
gattgcacgc ctgcctcca gctgggtga cagagcagc ctcctttca aataaataa 1560
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aaaaaa 1626

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<210> 48

<211> 368

<212> FRT

<213> Homo sapiens

<400> 48

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Met Ile Leu Pro Lys Arg Asn Leu Asn Glu Leu Trp Asn Phe Leu Phe
  1           5           10           15

Gly Glu Leu Ser Ala Val Phe Ala Phe Leu Arg Phe Gln Met Arg Val
          20           25           30

Tyr Ile Phe Leu Cys Leu Met Cys Trp Val Arg Ser Asp Asn Lys Arg
          35           40           45

Pro Cys Leu Glu Phe Ser Gln Leu Ser Val Lys Asp Ser Phe Arg Asp
          50           55           60

Leu Phe Ile Pro Arg Ile Glu Thr Ile Leu Met Met Tyr Thr Arg Asn
          65           70           75           80

Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu Asn
          85           90           95

Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly Tyr
          100          105          110

Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg Ile
          115          120          125

Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser Arg
          130          135          140

Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg Lys
          145          150          155          160

Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His Gly
          165          170          175

Ala Ser Leu Asp Asn Phe His Phe Ile Gly Val Ser Leu Gly Ala His
          180          185          190

Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg Ile
          195          200          205

Thr Gly Leu Asp Pro Ala Gly Pro Arg Phe Ser Arg Lys Pro Pro Tyr
          210          215          220

Ser Arg Leu Asp Tyr Thr Asp Ala Lys Phe Val Asp Val Ile His Ser
          225          230          235          240

Asp Ser Asn Gly Ile Gln Phe Ile Lys Cys Asn His Gln Arg Ala Val
          245          250          255

His Leu Phe Met Ala Ser Leu Glu Thr Asn Cys Asn Phe Ile Ser Phe

```

260	265	270
Pro Cys Arg Ser Tyr Lys Asp	Tyr Lys Thr Ser	Leu Lys Val Asp Cys
275	280	285
Asp Cys Phe Lys Glu Lys Ser	Cys Pro Arg Leu	Gly Tyr Gln Ala Lys
290	295	300
Leu Phe Lys Gly Val Leu Lys Glu	Arg Met Glu Gly Arg Pro	Leu Arg
305	310	315 320
Thr Thr Val Phe Leu Asp Thr	Ser Ala Tyr Tyr	Phe Val Leu Ser Ile
325	330	335
Ile Val Pro Asp Lys Thr Met Met	Asp Gly Ser Phe Ser	Phe Lys Leu
340	345	350
Leu Asn Gln Leu Gly Met Ile Glu	Glu Pro Arg Leu Tyr Glu	Glu Arg
355	360	365

<210> 49
 <211> 1221
 <212> DNA
 <213> Homo sapiens

<400> 49
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 agtgcacatga agaactacga gattagcctg gatattaact tctcttctag agaataagatt 180
 tcatgttcca tctctctgca atggttaatt cacacagaaa ccccatgttt acattccaa 240
 gaggatttta ctgcttaaca gccatcttgc ccccaatatg catttgttct cagttctcag 300
 tgcactctag ctatcacttc actgaggctc ctggggcctt cccagtagcc actaatgggg 360
 aacgatttcc ttggcaggag ctaaggctcc ctagtgtggt catctctctc cattatgacc 420
 tctttgtcca ccccaatctc acctctctgg cctttgttgc atctgagaag atcgaggtct 480
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 ccccccctca gtacagaggaa gattcagat acatgaaacc aggaanaagaa ctgaaagtgt 600
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 ccatctatgc atccccagac aaacgggaat aaacacatta tcttttgcag gcctcactga 960
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 caaananaaa aaaaaaaaaa a 1221

<210> 50
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 50
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 Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile
 20 25 30

Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu
 35 40 45
 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp
 50 55 60
 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu
 65 70 75 80
 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys
 85 90 95
 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser
 100 105 110
 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser
 115 120 125
 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala
 130 135 140
 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu
 145 150 155 160
 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe
 165 170 175
 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg
 180 185 190
 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe
 195 200 205
 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile
 210 215 220
 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Ser
 225 230 235 240
 Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln
 245 250 255
 Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr
 260 265 270
 Tyr Pro Leu Ser Lys Leu Gly Met Phe Lys Phe His Ile Ile Val Phe
 275 280 285
 Ile Phe Ala His Lys Thr Cys Leu Asp Leu Phe Pro Leu Ser Leu Cys
 290 295 300

Met
305

<210> 51
 <211> 951
 <212> DNA
 <213> Homo sapiens

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<400> 51
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cggtaacctc cccccagcac caccctccag cctctcpcct cggaggccag cagtggggag 240
gaagaatgcc ggtaacagcc caggagcacc agcgagagct ttctaacctg ccaaggtgct 300
gccccttttc taccacgggg aattggctca tccacaccac gaatcagcca cagcgggaac 360
aagcatgcag gggtctctca acagccttcc caagcaatgt tccctttact ccccccagaa 420
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gtagtgggtt ccactaatgg tagacaaagc actgaaagaa gtatcgctct aggaatggat 540
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ctatttcatt tggatggtsa tggtaggttc agtgtataga cggataaccg agttccata 660
tccaaacctg tatctgtgca gcaatgtgg gttagacagg attcaaggaa caaacactgt 720
gatgtactat tggtaggaag atgaactgga gcagccttcc tggagagtga ttgccaata 780
tgccttatca ttltgcctga tctttgtcct agtaactcta tctctatgga tttactctaa 840
gtttgttaac atggatgtgt gcaagattt tagctctaac aatgtttgtc agtgttctaa 900
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<210> 52

<211> 194

<212> PRT

<213> Homo sapiens

<400> 52

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Met Ala Leu Val Thr Val Gln Arg Ser Pro Thr Pro Ser Thr Thr Ser
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Ser Pro Cys Ala Ser Glu Ala Asp Ser Gly Glu Glu Glu Cys Arg Ser
          20              25              30

Gln Pro Arg Ser Ile Ser Glu Ser Phe Leu Thr Val Lys Gly Ala Ala
          35              40              45

Leu Phe Leu Pro Arg Gly Asn Gly Ser Ser Thr Pro Arg Ile Ser His
          50              55              60

Arg Arg Asn Lys His Ala Gly Asp Leu Gln Gln His Leu Gln Ala Met
          65              70              75              80

Phe Ile Leu Leu Arg Pro Glu Asp Asn Ile Arg Leu Ala Val Arg Leu
          85              90              95

Glu Ser Thr Tyr Gln Asn Arg Thr Arg Tyr Met Val Val Val Ser Thr
          100              105              110

Asn Gly Arg Gln Asp Thr Glu Glu Ser Ile Val Leu Gly Met Asp Phe
          115              120              125

Ser Ser Asn Asp Ser Thr Cys Thr Met Gly Leu Val Leu Pro Leu Trp
          130              135              140

Ser Asp Thr Leu Ile His Leu Asp Gly Asp Gly Gly Phe Ser Val Ser
          145              150              155              160

Thr Asp Asn Arg Val His Ile Phe Lys Pro Val Ser Val Gln Ala Met
          165              170              175

Trp Val Asp Arg Asp Ser Arg Asn Lys His Cys Asp Val Leu Leu Val
          180              185              190

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Glu Glu

<210> 53
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 53
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 gattttcggg ttttttcaca ttgcgctatt cagtataaac ctgctctcaa cattcatgtg 180
 caagtctttg agtgcacata tatttgcggt tctcttgagt gaatgcacct tgttgggtca 240
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 ttgcacatgt ttgttcaaat tcttcacctg tttttaaaga agcagtaaga cttatttttg 420
 tgttctgaac ataggttctt tctcacataa aatgtgctat gaatgttgag tttaaaatca 480
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 gaaacacatg tagctgggtt tactagtgaa atttgagttt taantgtcaa tgttagctaa 660
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 aatcacctag gtgtggcgcg ggcacgggtg ctacagcctg tggccccage actttgggac 1260
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 ccaattactc gggaggtctc agcaggagag tggcatgaac cggggagggc gattttgcat 1440
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 aaaaaaaaaa aaaa 1514

<210> 54
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 54
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 1 5 10 15
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 20 25 30
 Pro Leu His Phe Tyr Phe Phe Ile Gln Gln Val Leu Ile Lys Cys Ala
 35 40 45
 Leu Tyr Gln Val Leu Ser Ser Ser Leu Gly Tyr Asn Gly Asp Gln Gly
 50 55 60
 Asp Cys Arg Phe Trp Gln Gly Lys Leu Thr Ser Asn Thr Ala Thr Arg
 65 70 75 80
 His Ser Glu Thr Leu Ser Leu Leu Glu Glu Leu

<210> 55
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<400> 55

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tagcccaaga agcatctttt gcagacacga actcaatttc tccacttcag tcaacatcaa 240
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agcactcaat agttccatg cagagtaact ctccatccca ggaacagcag cagcagcagc 480
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aaaatccat ggtatccag gagcaacaga accagtcaat tttccacca caagtaaca 660
tggccccaat gaatcaagc caacagcccc tgcatttca gactcagtc acagtttct 720
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1417

<210> 56
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 56

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Met Gln Pro Pro Met Phe His Ser Gln Ser Thr Ile Ala Val Leu Gln
  1             5             10             15

Gly Ser Ser Val Pro Gln Asp Gln Gln Ser Thr Asn Ile Phe Leu Ser
      20             25             30

Gln Ser Pro Met Asn Asn Leu Gln Thr Asn Thr Val Ala Gln Glu Ala
      35             40             45

Phe Phe Ala Ala Pro Asn Ser Ile Ser Pro Leu Gln Ser Thr Ser Asn
      50             55             60

Ser Glu Gln Gln Ala Ala Phe Gln Gln Gln Ala Pro Ile Ser His Ile
      65             70             75             80

Gln Thr Pro Met Leu Ser Gln Glu Gln Ala Gln Pro Pro Gln Gln Gly
      85             90             95

Leu Phe Gln Pro Gln Val Ala Leu Gly Ser Leu Pro Pro Asn Pro Met
      100             105             110

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Pro Gln Ser Gln Gln Gly Thr Met Phe Gln Ser Gln His Ser Ile Val
 115 120 125
 Ala Met Gln Ser Asn Ser Pro Ser Gln Glu Gln Gln Gln Gln Gln
 130 135 140
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Ile Leu Phe Ser
 145 150 155 160
 Asn Gln Asn Thr Met Ala Thr Met Ala Ser Pro Lys Gln Pro Pro Pro
 165 170 175
 Asn Met Ile Phe Asn Pro Asn Gln Asn Pro Met Ala Asn Gln Glu Gln
 180 185 190
 Gln Asn Gln Ser Ile Phe His Gln Gln Ser Asn Met Ala Pro Met Asn
 195 200 205
 Gln Glu Gln Gln Pro Met Gln Phe Gln Ser Gln Ser Thr Val Ser Ser
 210 215 220
 Leu Gln Asn Pro Gly Pro Thr Gln Ser Glu Ser Ser Gln Thr Pro Leu
 225 230 235 240
 Phe His Ser Ser Pro Gln Ile Gln Leu Val Gln Gly Ser Pro Ser Ser
 245 250 255
 Gln Gln Gln Gln Val Thr Leu Phe Leu Ser Pro Ala Ser Met Ser Ala
 260 265 270
 Leu Gln Thr Ser Ile Asn Gln Gln Asp Met Gln Gln Ser Pro Leu Tyr
 275 280 285
 Ser Pro Gln Asn Asn Met Pro Gly Ile Gln Gly Ala Thr Phe Ser Pro
 290 295 300
 Gln Pro Gln Ala Thr Leu Phe His Asn Thr Ala Gly Gly Thr Met Asn
 305 310 315 320
 Gln Leu Gln Asn Ser Pro Gly Ser Ser Gln Gln Thr Ser Gly Met Phe
 325 330 335
 Leu Phe Gly Ile Gln Asn Asn Cys Ser Gln Leu Leu Thr Ser Gly Pro
 340 345 350
 Ala Thr Leu Pro Asp Gln Leu Met Ala Ile Ser Gln Pro Gly Gln Pro
 355 360 365
 Gln Asn Glu Gly Gln Pro Pro Val Thr Thr Leu Leu Ser Gln Gln Met
 370 375 380
 Pro Glu Asn Ser Pro Leu Ala Ser Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Glu Lys Ile Asp Leu Leu Val Ser Leu Gln Asn Gln Gly Asn Asn Leu
 405 410 415
 Thr Gly Ser Phe
 420

<210> 57
 <211> 2297
 <212> DNA
 <213> Homo sapiens

<400> 57
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 ttctgtggcta ctthgggga acaattgctc tgaactttgg atttttggag tatttcactt 180
 ttgcattaat ccccatgggt gtcatgggt taacttaata cttgtttgtg tgggaagact 240
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 taattctgaa agtttttagt ttaacttccc caaattgctt tgcctcactc tcttatattg 780
 cttttgtctt gaagatatg aagtttttgc gccagagctt ggcacacttc cttaattact 840
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 gtgtgcaggt gaagaggaa gctgcaggct taaaggcaga cattgatgct scatttatg 960
 aacaagtcat cctggaaaaa gaaatgggaa cttatttggg cactcttgat gattacttgg 1020
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<210> 58
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 <212> PRT
 <213> Homo sapiens

<400> 58
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 Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu Pro Arg Pro Gly Phe
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 His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly Lys Glu Glu Pro Leu
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 Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr Leu Val Ser Leu Pro
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 Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr Val Met Met Ile Tyr
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 Phe Asp Met Glu Val Trp Ala Leu Gly Leu His Glu Asn Ser Gly Ser
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 Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser Ile Ile Tyr Ala Ile
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 Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr Ala Ala Glu Phe Leu
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 Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala Tyr Gln Asn His Leu
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 Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys Leu Leu Arg Gln Ser
 195 200 205
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 Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His Gly Val Gln Val Lys
 225 230 235 240
 Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp Ala Thr Leu Tyr Glu
 245 250 255
 Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr Leu Gly Thr Phe Asp
 260 265 270
 Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr Val Ser Leu Phe Ser
 275 280 285
 Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val Leu Asn Asn Phe Thr
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 Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg Val Phe Lys Arg Pro
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 Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp Gln Met Ile Phe Cys
 325 330 335
 Leu Asp Thr Gly Val Lys Arg Gly Leu Asn Cys Lys Val Met Arg Asn
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Leu Leu Gly Glu Met Glu Met Ser Cys Val Leu Phe Val Val Val Val
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Val Ser Gln Val Asn Thr Pro Ile Lys Arg
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<210> 59

<211> 4145

<212> DNA

<213> Homo sapiens

<400> 59

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<210> 60

<211> 289

<212> PRT

<213> Homo sapiens

<400> 60

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Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr Gly Gly Leu
      20             25             30

Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys
      35             40             45

Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn
      50             55             60

Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala
      65             70             75             80

Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys
      85             90             95

Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys
      100            105            110

Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys
      115            120            125

Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro
      130            135            140

Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala Pro Thr Pro
      145            150            155            160

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Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro Gln Pro Pro
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Ala Arg Pro Pro Pro Val Leu Pro Ala Asn Arg Ala Pro Ser Ala
 180 185 190

Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro Ala Pro Ser
 195 200 205

Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr
 210 215 220

Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met
 225 230 235 240

Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro
 245 250 255

Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln
 260 265 270

Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln
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<210> 61
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<400> 61
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<210> 62

<211> 414

<212> PRT

<213> Homo sapiens

<400> 62

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Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
35 40 45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
50 55 60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
65 70 75 80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
85 90 95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
100 105 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
115 120 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
130 135 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
145 150 155 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
165 170 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
180 185 190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
195 200 205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
210 215 220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
225 230 235 240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
245 250 255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
275 280 285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn

290	295	300
Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly		
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Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Ser Arg Ala Gly		
	325	330 335
Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val		
	340	345 350
Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly		
	355	360 365
Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys		
	370	375 380
Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu		
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<210> 63
 <211> 1571
 <212> DNA
 <213> Homo sapiens

<400> 63

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<210> 64
 <211> 417

<212> PRT

<213> Homo sapiens

<400> 64

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      20             25             30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
      35             40             45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
      50             55             60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
      65             70             75             80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
      85             90             95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
      100             105             110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
      115             120             125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
      130             135             140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys
      145             150             155             160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu
      165             170             175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu
      180             185             190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu
      195             200             205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu
      210             215             220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro
      225             230             235             240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu
      245             250             255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu
      260             265             270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu
      275             280             285

Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val
      290             295             300

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Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu
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Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr Lys Lys Ala Leu
325 330 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys
340 345 350

Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Glu Asp Ile Leu
355 360 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Glu Thr Gly Arg Ile
370 375 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp
385 390 395 400

Val Gly Lys Thr Glu Pro Pro Leu Met Lys Arg Ala Phe Ser Thr Glu
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<210> 65
<211> 1752
<212> DNA
<213> Homo sapiens

<400> 65
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gctccagaaa caggaccagg accgcatgta tttctctctc ttctgaaagt tctgcttgt 1560
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taaatagggc tccctggtat ctctgtctt cctactgtt caaaccccta aattttggtt 1680

gtacatttta ttggaaggga aaataaattt tttttttggg ccaaaagaaa aaaaaaaa 1740
 aaaaaaaa aa 1752

<210> 66
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Tyr Gln Val Pro Leu Pro Leu Asp Arg Asp Gly Thr Leu Val Arg
 1 5 10 15
 Leu Arg Phe Thr Met Val Ala Leu Val Thr Val Cys Cys Pro Leu Val
 20 25 30
 Ala Phe Leu Phe Cys Ile Leu Trp Ser Leu Leu Phe His Phe Lys Glu
 35 40 45
 Thr Thr Ala Thr His Cys Gly Val Pro Asn Tyr Leu Pro Ser Val Ser
 50 55 60
 Ser Ala Ile Gly Gly Glu Val Pro Gln Arg Tyr Val Trp Arg Phe Cys
 65 70 75 80
 Ile Gly Leu His Ser Ala Pro Arg Phe Leu Val Ala Phe Ala Tyr Trp
 85 90 95
 Asn His Tyr Leu Ser Cys Thr Ser Pro Cys Ser Cys Tyr Arg Pro Leu
 100 105 110
 Cys Arg Leu Asn Phe Gly Leu Asn Val Val Glu Asn Leu Ala Leu Leu
 115 120 125
 Val Leu Thr Tyr Val Ser Ser Ser Glu Asp Phe Thr Ile His Glu Asn
 130 135 140
 Ala Phe Ile Val Phe Ile Ala Ser Ser Leu Gly His Met Leu Leu Thr
 145 150 155 160
 Cys Ile Leu Trp Arg Leu Thr Lys Lys His Thr Val Ser Gln Glu Asp
 165 170 175
 Arg Lys Ser Tyr Ser Trp Lys Gln Arg Leu Phe Ile Ile Asn Phe Ile
 180 185 190
 Ser Phe Phe Ser Ala Leu Ala Val Tyr Phe Arg His Asn Met Tyr Cys
 195 200 205
 Glu Ala Gly Val Tyr Thr Ile Phe Ala Ile Leu Glu Tyr Thr Val Val
 210 215 220
 Leu Thr Asn Met Ala Phe His Met Thr Ala Trp Trp Asp Phe Gly Asn
 225 230 235 240
 Lys Glu Leu Leu Ile Thr Ser Gln Pro Glu Glu Lys Arg Phe
 245 250

<210> 67
 <211> 782

<212> DNA

<213> Homo sapiens

<400> 67

```

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taaaacacac agtttagtaa ccttttttat gctttggaat accatgatgg caccatctct 180
actaagcatt ccttggggca taaaacagge tggctttact acctggaatgt gtgtcatcat 240
actgatgggc cttttaacac ttctattgctg ctacagagta gtgaaatcac ggactatgat 300
gttttcattg gataccacta cctgggaata tcccgatgtc tgcagacatt atttcggctc 360
ctttgggcag tggtcagtc tctctctctc cttggtgtct ctcatggag caatgatagt 420
ttattgggtg ctctatgtca atttctttt taatactgga aggtttattt ttagtaagta 480
tctatcatcat atgcttttaa cccagtactt tcaatacta ttccacctgt aatgttagtt 540
ctagccttaa attccaggac ttgggataaa taataaaga agtaacatat ataattttgg 600
aaatatatc ttattcagtc ggctttctgt gtttgtgctc tcaatatag tgtatgctta 660
tttccaaaca ttaattcttg aaggaataat atctctccaa atcttttagt taatatanaa 720
tatgtctata atccaaaaa aaaaaaana aaaaaaana aaaaaaana aaaaaaana 780

```

<210> 68

<211> 127

<212> PRT

<213> Homo sapiens

<400> 68

```

Met Ile Trp Asn Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp
  1             5             10             15
Gly Ile Lys Gln Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu
          20             25             30
Met Gly Leu Leu Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg
          35             40             45
Thr Met Met Phe Ser Leu Asp Thr Thr Thr Trp Glu Tyr Pro Asp Val
          50             55             60
Cys Arg His Tyr Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe
          65             70             75             80
Ser Leu Val Ser Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met
          85             90             95
Ser Asn Phe Leu Phe Asn Thr Gly Lys Phe Ile Phe Ser Lys Tyr Leu
          100            105            110
Tyr His Met Leu Leu Thr Gln Tyr Phe Gln Ile Leu Leu Pro Leu
          115            120            125

```

<210> 69

<211> 649

<212> DNA

<213> Homo sapiens

<400> 69

```

gagcaactcc ctcccccac tctgctcccc atgtggacgc tgaatctgtc cctggctctg 60
cttctgtgac taccctgacg ctatgccttc atgtctcttt ctctggagaa gaaaactagc 120
gaaccccagg ggaaggtgca atcaggagag cacttkagga ttgggcagaa tctccagag 180
cacacccaag gcttggcttg gagcaaatgg ctctggcttc ttttggttgt tgtgccttt 240

```

```

gtgatactgc agtgtcaaaag agacagtgag aagaataagg agcagaagtc tectggccct 300
cggggggggc aacttcactc tccattaaaag aaaaaaangaa atgcttcccc caacaagagc 360
tgtgcattca atacttaac ggaactcgag gtggagccta tgaatttgt gtccaaagtg 420
cggaaatetta aacgtgccat ggaacagggt agtggcagta accdcagggt tcgaaagtc 480
gagatgcctg tagatccata ccatgtcaag atctgtgaaa tatggggaga agaaagctct 540
agctgaatgg atttgtgtgt caggagagaa aaaaagttag tgttgacaaa ctgtatgaa 600
actaataaa ctattctgaa gaaaagaaaa aaaaaaanaa aaaaaaaa 649

```

<210> 70

<211> 171

<212> PRT

<213> Homo sapiens

<400> 70

```

Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys
  1              5              10              15

Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro
          20              25              30

Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu
          35              40              45

Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu
  50              55              60

Phe Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu
  65              70              75              80

Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His
          85              90              95

Ser Pro Leu Lys Lys Lys Arg Asn Ala Ser Pro Asn Lys Asp Cys Ala
        100              105              110

Phe Asn Thr Leu Met Glu Leu Glu Val Glu Leu Met Lys Phe Val Ser
        115              120              125

Lys Val Arg Asn Leu Lys Arg Ala Met Ala Thr Gly Ser Gly Ser Asn
        130              135              140

Leu Arg Leu Arg Lys Ser Glu Met Pro Ala Asp Pro Tyr His Val Thr
        145              150              155              160

Ile Cys Glu Ile Trp Gly Glu Glu Ser Ser Ser
          165              170

```

<210> 71

<211> 1456

<212> DNA

<213> Homo sapiens

<400> 71

```

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tcgggcaactc gtctcacctg ggaatgtcat cactcaaaa atgagggagag ctggcacgat 120
gggtgcccggc aatgtactctg tctcaatgga cgggaaatgt gtgacctgat caactgcccg 180
gtgcttgccct gtggcaaccr cccattccac cctggacagt gctgcccata atgtgcagat 240
gactttgttg tgcagaagcc agagctcagt actccctca ttgcccacgt cctggagaga 300
gaataactttg tggaaaggaga aacgtggaac attgaactct gtactcagtg cacttgccac 360

```

```

agcggagcggg tgcctgtgtga gacagaggtg tgcacacgcg tgcctctgcca gaacccctca 420
cgcccccagg attcctgctg cccacagtgt acagatcacc cttcttggcc ttccctgtcc 480
cgcaataaca gcttacctaa ttattgcaaa atgagtgaag gggatatatt cctggcagct 540
gagtcctgga agcctgacgt ttgtaccagg tgcctctgca ttgatagcgt aattagctgt 600
ttctctgagt cctgaccttc tgtatcctgt gaagacctg tcttgagaaa aggcagtggt 660
tgtccctact gcctagagaa cacaattcca aagaagggtg tgtccacctt cagtgggaag 720
gcctatgccc acgaggagcg gtgggacctt gacagctgca cctactgata ctgcttgag 780
ggccagaccc tctgctcgac cgtcagctgc cccctctgct cctgtgttga gcccatcaac 840
gtgggaaggaa gttgctgccc aatgtgtcca gaaatgtatg tcccagaacc aaccaatata 900
cccattgaga agacaaacca tggaggagag gttagcctgg aggttccctt gtggcccccg 960
cctagtgaaa atgatctgt ccatctccct agagatatgg gtacccctca ggtagattac 1020
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aaccatctac aggcagacaa ttctaccaa acagtgtaga gaagggcanc taggatgag 1380
tttcaaaaga cgggaagcga ctcaatctgc tctaaaagt aaactagact ttgtgcactt 1440
aaaaaaauuu aaaaaa

```

<210> 72

<211> 400

<212> PRT

<213> Homo sapiens

<400> 72

```

Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr
  1             5             10             15

```

```

Ile His Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val
      20             25             30

```

```

Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly
      35             40             45

```

```

Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln
      50             55             60

```

```

Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro
      65             70             75             80

```

```

Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro
      85             90             95

```

```

Gln Cys Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser
     100             105             110

```

```

Val Pro Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala
     115             120             125

```

```

Glu Ser Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser
     130             135             140

```

```

Val Ile Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg
     145             150             155             160

```

```

Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr
     165             170             175

```

```

Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp

```

180					185					190					
Glu	Glu	Arg	Trp	Asp	Leu	Asp	Ser	Cys	Thr	His	Cys	Tyr	Cys	Leu	Gln
		295					300					205			
Gly	Gln	Thr	Leu	Cys	Ser	Thr	Val	Ser	Cys	Pro	Pro	Leu	Pro	Cys	Val
	210					215					220				
Glu	Pro	Ile	Asn	Val	Glu	Gly	Ser	Cys	Cys	Pro	Met	Cys	Pro	Glu	Met
225				230						235				240	
Tyr	Val	Pro	Glu	Pro	Thr	Asn	Ile	Pro	Ile	Glu	Lys	Thr	Asn	His	Arg
				245					250					255	
Gly	Glu	Val	Asp	Leu	Glu	Val	Pro	Leu	Trp	Pro	Thr	Pro	Ser	Glu	Asn
		260					265						270		
Asp	Ile	Val	His	Leu	Pro	Arg	Asp	Met	Gly	His	Leu	Gln	Val	Asp	Tyr
	275						280					285			
Arg	Asp	Asn	Arg	Leu	His	Pro	Ser	Glu	Asp	Ser	Ser	Leu	Asp	Ser	Ile
	290					295					300				
Ala	Ser	Val	Val	Val	Pro	Ile	Ile	Ile	Cys	Leu	Ser	Ile	Ile	Ile	Ala
305				310					315						320
Phe	Leu	Phe	Ile	Asn	Gln	Lys	Lys	Gln	Trp	Ile	Pro	Leu	Leu	Cys	Trp
			325					330						335	
Tyr	Arg	Thr	Pro	Thr	Lys	Pro	Ser	Ser	Leu	Asn	Asn	Gln	Leu	Val	Ser
		340						345					350		
Val	Asp	Cys	Lys	Lys	Gly	Thr	Arg	Val	Gln	Val	Asp	Ser	Ser	Gln	Arg
	355						360					365			
Met	Leu	Arg	Ile	Ala	Glu	Pro	Asp	Ala	Arg	Phe	Ser	Gly	Phe	Tyr	Ser
	370					375					380				
Met	Gln	Lys	Gln	Asn	His	Leu	Gln	Ala	Asp	Asn	Phe	Tyr	Gln	Thr	Val
385				390					395						400

<210> 73

<211> 4723

<212> DNA

<213> Homo sapiens

<400> 73

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ggccttcacg ggcctatcttt tttttttttt aaatgataca acttaatttt attaggacaa 60
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ggatgctact cgggcaccta gaagccacag ctgccttcca cagagcgcca ctgcactatg 180
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gcgaacatac tctgaggaa ccgtacgggc tccagccacg actcgatgag cagcagggag 480
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atagagtcct agaagcagaa ggaggtcttg gactcatgca ggaatgaata cttctggctc 600
tttgagatat aggtttcttc aaactccttg taggtgtcaa tggcccgctg gtgcgcgcga 660
tggtgttgga gcatacgctg gtcaaaaagc ctggataacg gaacgggttg gatggaccca 720

```

```

gectottttaa gcccagggcag gcagagcaggy gcaaaagccaa ggagcagggga cgtccggggag 780
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```



```

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```

<210> 74

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 74

```

Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
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Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
      20             25             30

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35             40             45

Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50             55             60

Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65             70             75             80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85             90             95

Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
     100             105             110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
     115             120             125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
     130             135             140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
     145             150             155             160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
     165             170             175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
     180             185             190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
     195             200             205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
     210             215             220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
     225             230             235             240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg

```

245	250	255
Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Cys Pro Pro Asp Ser 260 265 270		
Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Thr Leu Pro 275 280 285		
Thr Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys Glu 290 295 300		
Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly 305 310 315 320		
Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys 325 330 335		
Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp 340 345 350		
Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr 355 360 365		
Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly 370 375 380		
Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn Pro 385 390 395 400		
Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp 405 410 415		
Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His 420 425 430		
Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val 435 440 445		
Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val 450 455 460		
Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Gly Lys 465 470 475 480		
Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr Cys 485 490 495		
Gln Cys Ile Asn Thr Glu Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys 500 505 510		
Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu 515 520 525		
Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys 530 535 540		
Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp 545 550 555 560		
Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys		

565										570					575				
Pro	Leu	Gly	Phe	Gln	Gln	Asp	Ser	His	Gly	Cys	Leu	Ile	Cys	Lys	Cys				
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Glu	Gly	Glu	Thr	Trp	Asn	Ile	Asp	Ser	Cys	Thr	Gln	Cys	Thr	Cys	His				
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Ser	Gly	Arg	Val	Leu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Pro	Leu	Leu	Cys				
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Gln	Asn	Pro	Ser	Arg	Thr	Gln	Asp	Ser	Cys	Cys	Pro	Gln	Cys	Thr	Asp				
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Gln	Pro	Phe	Arg	Pro	Ser	Leu	Ser	Arg	Asn	Asn	Ser	Val	Pro	Asn	Tyr				
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Cys	Lys	Asn	Asp	Glu	Gly	Asp	Ile	Phe	Leu	Ala	Ala	Glu	Ser	Trp	Lys				
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Pro	Asp	Val	Cys	Thr	Ser	Cys	Ile	Cys	Ile	Asp	Ser	Val	Ile	Ser	Cys				
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Phe	Ser	Glu	Ser	Cys	Pro	Ser	Val	Ser	Cys	Glu	Arg	Pro	Val	Leu	Arg				
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Lys	Gly	Gln	Cys	Cys	Pro	Tyr	Cys	Ile	Glu	Asp	Thr	Ile	Pro	Lys	Lys				
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Asp	Leu	Asp	Ser	Cys	Thr	His	Cys	Tyr	Cys	Leu	Gln	Gly	Gln	Thr	Leu				
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Cys	Ser	Thr	Val	Ser	Cys	Pro	Pro	Leu	Pro	Cys	Val	Glu	Pro	Ile	Asn				
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Val	Glu	Gly	Ser	Cys	Cys	Pro	Met	Cys	Pro	Glu	Met	Tyr	Val	Pro	Glu				
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Pro	Thr	Asn	Ile	Pro	Ile	Glu	Lys	Thr	Asn	His	Arg	Gly	Glu	Val	Asp				

865 890 895

Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn Asp Ile Val His
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Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg
915 920 925

Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val
930 935 940

Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile
945 950 955 960

Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro
965 970 975

Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys
980 985 990

Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile
995 1000 1005

Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser Met Gln Lys Gln
1010 1015 1020

Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val
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<210> 75
<211> 3862
<212> DNA
<213> Homo sapiens

<400> 75

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<210> 76

<211> 457

<212> PRT

<213> Homo sapiens

<400> 76

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Leu Phe Phe Leu Leu Leu Glu Gly Lys Lys Thr Glu Gln Val Lys His
          20             25             30
Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
          35             40             45
Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
          50             55             60

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Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys
 65 70 75 80
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys
 85 90 95
 Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser
 100 105 110
 Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe
 115 120 125
 Val Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Glu Cys Thr Gln
 130 135 140
 Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro
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 Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg
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 Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp
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 Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg
 195 200 205
 Ser His Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg
 210 215 220
 Phe Pro Gly Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln
 225 230 235 240
 Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His
 245 250 255
 Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser
 260 265 270
 Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys
 275 280 285
 Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn
 290 295 300
 Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys
 305 310 315 320
 Val Cys Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe
 325 330 335
 Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu
 340 345 350
 Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu
 355 360 365
 Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys
 370 375 380

Gly Ile Leu Gln His Phe His Ile Glu Lys Tle Ser Lys Arg Met Phe
 395 390 395 400

Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln
 405 410 415

Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser
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Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr
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Leu Glu Arg Ser Glu Lys Gly His Cys
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<210> 77

<211> 2050

<212> DNA

<213> Homo sapiens

<400> 77

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<210> 78

<211> 505

<212> PRT

<213> Homo sapiens

<400> 78

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Lys Asn Cys Trp Arg Ile Lys Lys Gly Phe Val Pro Asn Met Gln Val
          20           25           30

Glu Gly Val Phe Tyr Val Asn Asp Ala Leu Glu Lys Leu Met Phe Glu
          35           40           45

Glu Leu Arg Asn Ala Cys Arg Gly Gly Gly Val Gly Gly Phe Leu Pro
 50           55           60

Ala Met Lys Gln Ile Gly Asn Val Ala Ala Leu Pro Gly Ile Val His
 65           70           75           80

Arg Ser Ile Gly Leu Pro Asp Val His Ser Gly Tyr Gly Phe Ala Ile
          85           90           95

Gly Asn Met Ala Ala Phe Asp Met Asn Asp Pro Glu Ala Val Val Ser
          100          105          110

Pro Gly Gly Val Gly Phe Asp Ile Asn Cys Gly Val Arg Leu Leu Arg
          115          120          125

Thr Asn Leu Asp Glu Ser Asp Val Gln Pro Val Lys Glu Gln Leu Ala
          130          135          140

Gln Ala Met Phe Asp His Ile Pro Val Gly Val Gly Ser Lys Gly Val
          145          150          155          160

Ile Pro Met Asn Ala Lys Asp Leu Glu Glu Ala Leu Glu Met Gly Val
          165          170          175

Asp Trp Ser Leu Arg Glu Gly Tyr Ala Trp Ala Glu Asp Lys Glu His
          180          185          190

Cys Glu Glu Tyr Gly Arg Met Leu Gln Ala Asp Pro Asn Lys Val Ser
          195          200          205

Ala Arg Ala Lys Lys Arg Gly Leu Pro Gln Leu Gly Thr Leu Gly Ala
          210          215          220

Gly Asn His Tyr Ala Glu Ile Gln Val Val Asp Glu Ile Phe Asn Glu
          225          230          235          240

Tyr Ala Ala Lys Lys Met Gly Ile Asp His Lys Gly Gln Val Cys Val
          245          250          255

Met Ile His Ser Gly Ser Arg Gly Leu Gly His Gln Val Ala Thr Asp
          260          265          270

Ala Leu Val Ala Met Glu Lys Ala Met Lys Arg Asp Lys Ile Ile Val
          275          280          285

Asn Asp Arg Gln Leu Ala Cys Ala Arg Ile Ala Ser Pro Glu Gly Gln
          290          295          300

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Asp Tyr Leu Lys Gly Met Ala Ala Ala Gly Asn Tyr Ala Trp Val Asn
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Arg Ser Ser Met Thr Phe Leu Thr Arg Gln Ala Phe Ala Lys Val Phe
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Asn Thr Thr Pro Asp Asp Leu Asp Leu His Val Ile Tyr Asp Val Ser
                      340                      345                      350

His Asn Ile Ala Lys Val Glu Gln His Val Val Asp Gly Lys Glu Arg
                      355                      360                      365

Thr Leu Leu Val His Arg Lys Gly Ser Thr Arg Ala Phe Pro Pro His
370                      375                      380

His Pro Leu Ile Ala Val Asp Tyr Gln Leu Thr Gly Gln Pro Val Leu
385                      390                      395                      400

Ile Gly Gly Thr Met Gly Thr Cys Ser Tyr Val Leu Thr Gly Thr Glu
                      405                      410                      415

Gln Gly Met Thr Glu Thr Phe Gly Thr Thr Cys His Gly Ala Gly Arg
                      420                      425                      430

Ala Leu Ser Arg Ala Lys Ser Arg Arg Asn Leu Asp Phe Gln Asp Val
435                      440                      445

Leu Asp Lys Leu Ala Asp Met Gly Ile Ala Ile Arg Val Ala Ser Pro
450                      455                      460

Lys Leu Val Met Glu Glu Ala Pro Glu Ser Tyr Lys Asn Val Thr Asp
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Val Val Asn Thr Cys His Asp Ala Gly Ile Ser Lys Lys Ala Ile Lys
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Leu Arg Pro Ile Ala Val Ile Lys Gly
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<210> 79

<211> 1178

<212> DNA

<213> Homo sapiens

<400> 79

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<210> 80

<211> 310

<212> PRT

<213> Homo sapiens

<400> 80

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      20                      25                      30

Leu Gly Lys Gly Val Lys His Arg Pro Pro Pro Ile Lys Leu Pro Ser
      35                      40                      45

Ser Ser Gly Asn Ser Ser Ser Gly Asn Tyr Phe Thr Pro Gln Gln Thr
      50                      55                      60

Ser Ser Phe Leu Lys Ser Pro Thr Pro Pro Pro Ser Ser Lys Pro Ser
      65                      70                      75                      80

Ser Ile Pro Arg Lys Ser Ser Val Asp Leu Asn Gln Val Ser Met Leu
      85                      90                      95

Ser Pro Ala Ala Leu Ser Pro Ala Ser Ser Ser Gln Arg Thr Thr Ala
      100                      105                      110

Thr Gln Val Met Ala Asn Ser Ala Gly Leu Asn Phe Ile Asn Val Val
      115                      120                      125

Gly Ser Val Cys Gly Ala Gln Ala Leu Met Ser Gly Ser Asn Pro Met
      130                      135                      140

Leu Gly Cys Asn Thr Gly Ala Ile Thr Pro Ala Gly Ile Asn Leu Ser
      145                      150                      155                      160

Gly Leu Leu Pro Ser Gly Gly Leu Leu Pro Asn Ala Leu Pro Ser Ala
      165                      170                      175

Met Gln Ala Ala Ser Gln Ala Gly Val Pro Phe Gly Leu Lys Asn Thr
      180                      185                      190

Ser Ser Leu Arg Pro Leu Asn Leu Leu Gln Leu Pro Gly Gly Ser Leu
      195                      200                      205

Ile Phe Asn Thr Leu Gln Gln Gln Gln Gln Leu Ser Gln Phe Thr
      210                      215                      220

Pro Gln Gln Pro Gln Gln Pro Thr Thr Cys Ser Pro Gln Gln Pro Gly
      225                      230                      235                      240

Glu Gln Gly Ser Glu Gln Gly Ser Thr Ser Gln Glu Gln Ala Leu Ser

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245	250	255
Ala Gln Gln Ala Ala Val Ile Asn Leu Thr Gly Val Gly Ser Phe Met		
260	265	270
Gln Ser Gln Ala Ala Ala Val Ala Ile Leu Ala Ala Ser Asn Gly Tyr		
275	280	285
Gly Ser Ser Ser Ser Thr Asn Ser Ser Ala Thr Ser Ser Ser Ala Tyr		
290	295	300
Arg Gln Pro Val Lys Lys		
305	310	

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 <211> 641
 <212> DNA
 <213> Homo sapiens

<400> B1
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 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> B2
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 Cys Leu Pro Leu Phe His Ser Ser Thr Leu Pro Tyr Met Glu Asp Lys
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 Trp Thr Pro Gly Val Leu Thr Leu Leu Val Pro Ala Pro Ala Tyr Pro
 35 40 45
 Arg Cys Gln Gln Thr Leu Val His Arg Arg Leu Pro Gln Leu Trp Ser
 50 55 60
 Gln Glu Arg Ile Ser Leu His Trp Met Asp Cys His Leu Arg Leu Lys
 65 70 75 80
 Ile Ile Phe Leu Ile Phe Leu Leu Ile Ser Met Leu Ser Leu
 85 90

<210> B3
 <211> B32

<212> DNA

<213> Homo sapiens

<400> 83

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tgtcatgaga ggaagaaaca agaatgaca gtgtatgact gcctttgagc tctagttccc 780
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<210> 84

<211> 140

<212> PRT

<213> Homo sapiens

<400> 84

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Ala Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe
      20             25             30

Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile
      35             40             45

Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr
      50             55             60

Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser
      65             70             75             80

Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu Pro Cys
      85             90             95

Tyr Gly His Gly Leu Ser Tyr Ser Val Pro Val Pro Asp Phe Ser Thr
      100            105            110

Asp Cys Leu His Ala Gly Leu Cys Arg Gly Ser Glu Leu Pro Pro Gly
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Trp Leu Pro Val Val Cys Pro Val Ser Gly Gly His Gln Pro Asp Tyr
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<210> 85

<211> 3790

<212> DNA

<213> Homo sapiens

<400> 85

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<210> 86
 <211> 940
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Leu Arg Leu Ser Phe Ser Glu Ile Asn Thr Arg Val Ile Lys Glu Asp
 35 40 45
 Ile Val Arg Arg Glu Arg Ile Gly Phe Arg Val Gln Pro Asp Gln Gly
 50 55 60
 Lys Ile Phe Tyr Ser Ser Ile Lys Glu Met Lys Pro Pro Leu Arg Gly
 65 70 75 80
 His Gly Lys Gly Ala Trp Gly Lys Glu Asn Val Arg Lys Thr Glu Glu
 85 90 95
 Ser Val Leu Lys Val Glu Val Asp Leu Asp Gln Thr Gln Arg Glu Arg
 100 105 110
 Lys Met Gln Asn Ala Leu Gly Arg Gly Lys Val Val Pro Leu Trp His
 115 120 125
 Pro Ala His Leu Gln Thr Leu Pro Val Thr Pro Asn Lys Gln Lys Thr
 130 135 140
 Asp Gly Arg Gly Thr Lys Pro Glu Ala Ser Ser His Gln Gly Thr Pro
 145 150 155 160
 Lys Gln Thr Thr Ala Gln Gly Ala Pro Lys Thr Ser Phe Ile Ala Ala
 165 170 175
 Lys Gly Thr Gln Val Val Lys Ile Ser Val His Met Gly Arg Val Ser
 180 185 190
 Leu Lys Gln Glu Pro Arg Lys Ser His Ser Pro Ser Ser Asp Thr Ser
 195 200 205
 Lys Leu Ala Ala Glu Arg Asp Leu Asn Val Thr Ile Ser Leu Ser Thr
 210 215 220
 Asp Arg Pro Lys Gln Arg Ser Gln Ala Val Ala Asn Glu Arg Ala His
 225 230 235 240
 Pro Ala Ser Thr Ala Val Pro Lys Ser Gly Glu Ala Met Ala Leu Asn
 245 250 255
 Lys Thr Lys Thr Gln Ser Lys Glu Val Asn Ala Asn Lys His Lys Ala
 260 265 270

Asn Thr Ser Leu Pro Phe Pro Lys Phe Thr Val Asn Ser Asn Arg Leu
 275 285
 Arg Lys Gln Ser Ile Asn Glu Thr Pro Leu Gly Ser Leu Ser Lys Asp
 290 295 300
 Asp Gly Ala Arg Gly Ala His Gly Lys Lys Leu Asn Phe Ser Glu Ser
 305 310 315 320
 His Leu Val Ile Ile Thr Lys Glu Glu Glu Gln Lys Ala Asp Pro Lys
 325 330 335
 Glu Val Ser Asn Ser Lys Thr Lys Thr Ile Phe Pro Lys Val Leu Gly
 340 345 350
 Lys Ser Gln Ser Lys His Ile Ser Arg Asn Arg Ser Glu Met Ser Ser
 355 360 365
 Ser Ser Leu Ala Pro His Arg Val Pro Leu Ser Gln Thr Asn His Ala
 370 375 380
 Leu Thr Gly Gly Leu Glu Pro Ala Lys Ile Asn Ile Thr Ala Lys Ala
 385 390 395 400
 Pro Ser Thr Glu Tyr Asn Gln Ser His Ile Lys Ala Leu Leu Pro Glu
 405 410 415
 Asp Ser Gly Thr His Gln Val Leu Arg Ile Asp Val Thr Leu Ser Pro
 420 425 430
 Arg Asp Pro Lys Ala Pro Gly Gln Phe Gly Arg Pro Val Val Val Pro
 435 440 445
 His Gly Lys Glu Lys Glu Ala Glu Arg Arg Trp Lys Glu Gly Asn Phe
 450 455 460
 Asn Val Tyr Leu Ser Asp Leu Ile Pro Val Asp Arg Ala Ile Glu Asp
 465 470 475 480
 Thr Arg Pro Ala Gly Cys Ala Glu Gln Leu Val His Asn Asn Leu Pro
 485 490 495
 Thr Thr Ser Val Ile Met Cys Phe Val Asp Glu Val Trp Ser Thr Leu
 500 505 510
 Leu Arg Ser Val His Ser Val Ile Asn Arg Ser Pro Pro His Leu Ile
 515 520 525
 Lys Glu Ile Leu Leu Val Asp Asp Phe Ser Thr Lys Asp Tyr Leu Lys
 530 535 540
 Asp Asn Leu Asp Lys Tyr Met Ser Gln Phe Pro Lys Val Arg Ile Leu
 545 550 555 560
 Arg Leu Lys Glu Arg His Gly Leu Ile Arg Ala Arg Leu Ala Gly Ala
 565 570 575
 Gln Asn Ala Thr Gly Asp Val Leu Thr Phe Leu Asp Ser His Val Glu
 580 585 590

Cys Asn Val Gly Trp Leu Glu Pro Leu Leu Glu Arg Val Tyr Leu Ser
 595 600 605
 Arg Lys Lys Val Ala Cys Pro Val Ile Glu Val Ile Asn Asp Lys Asp
 610 615 620
 Met Ser Tyr Met Thr Val Asp Asn Phe Gln Arg Gly Ile Phe Val Trp
 625 630 635 640
 Pro Met Asn Phe Gly Trp Arg Thr Ile Pro Pro Asp Val Ile Ala Lys
 645 650 655
 Asn Arg Ile Lys Glu Thr Asp Thr Ile Arg Cys Pro Val Met Ala Gly
 660 665 670
 Gly Leu Phe Ser Ile Asp Lys Ser Tyr Phe Phe Glu Leu Gly Thr Tyr
 675 680 685
 Asp Pro Gly Leu Asp Val Trp Gly Gly Glu Asn Met Glu Leu Ser Phe
 690 695 700
 Lys Val Trp Met Cys Gly Gly Glu Ile Glu Ile Ile Pro Cys Ser Arg
 705 710 715 720
 Val Gly His Ile Phe Arg Asn Asp Asn Pro Tyr Ser Phe Pro Lys Asp
 725 730 735
 Arg Met Lys Thr Val Glu Arg Asn Leu Val Arg Val Ala Glu Val Trp
 740 745 750
 Leu Asp Glu Tyr Lys Glu Leu Phe Tyr Gly His Gly Asp His Leu Ile
 755 760 765
 Asp Gln Gly Leu Asp Val Gly Asn Leu Thr Gln Gln Arg Glu Leu Arg
 770 775 780
 Lys Lys Leu Lys Cys Lys Ser Phe Lys Trp Tyr Leu Glu Asn Val Phe
 785 790 795 800
 Pro Asp Leu Arg Ala Pro Ile Val Arg Ala Ser Gly Val Leu Ile Asn
 805 810 815
 Val Ala Leu Gly Lys Cys Ile Ser Ile Glu Asn Thr Thr Val Ile Leu
 820 825 830
 Glu Asp Cys Asp Gly Ser Lys Gln Leu Gln Gln Phe Asn Tyr Thr Trp
 835 840 845
 Leu Arg Leu Ile Lys Cys Gly Glu Trp Cys Ile Ala Pro Ile Pro Asp
 850 855 860
 Lys Gly Ala Val Arg Leu His Pro Cys Asp Asn Arg Asn Lys Gly Leu
 865 870 875 880
 Lys Trp Leu His Lys Ser Thr Ser Val Phe His Pro Glu Leu Val Asn
 885 890 895
 His Ile Val Phe Glu Asn Asn Gln Gln Leu Leu Cys Leu Glu Gly Asn
 900 905 910

Phe Ser Gln Lys Ile Leu Lys Val Ala Ala Cys Asp Pro Val Lys Pro
 915 920 925

Tyr Gln Lys Trp Lys Phe Glu Lys Tyr Tyr Glu Ala
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<210> 87
 <211> 1200
 <212> DNA
 <213> Homo sapiens

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<210> 88
 <212> 286
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asp Lys Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser Glu Gly Gly
 50 55 60
 Pro Ala Glu Ile Ala Gly Leu Gln Ile Gly Asp Lys Ile Met Gln Val
 65 70 75 80
 Asn Gly Trp Asp Met Thr Met Val Thr His Asp Gln Ala Arg Lys Arg
 85 90 95
 Leu Thr Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val Thr Arg Gln

100	105	110
Ser Leu Glu Lys Ala Cys Ser Ser His Ala Val Leu Ala Ala Thr Thr		
115	120	125
Ile Cys Asp Ser Cys Leu Pro Pro Leu Cys Thr Val Thr Pro Leu Pro		
130	135	140
His Ser Val Pro Ile Trp Leu Leu Leu Thr Ser Phe Leu Ser Trp Thr		
145	150	155
Pro Arg Ile Gly Asn Lys Gly Leu Glu Leu Ser Ser Ser Gln Ser Ala		
165	170	175
Val Thr Thr Gly Ser Gly Pro Thr Leu Leu Leu Gly His Ser Ser Gly		
180	185	190
Trp Ala Ser Gly Asn His Tyr Leu Leu Gly Ala Pro Lys Ser Trp Glu		
195	200	205
Met Leu Glu Glu Pro Gly Leu Ser Arg Phe Cys Leu Ala Ala Gly Leu		
210	215	220
Gly Ser Ala Pro Ala Pro Gln Pro Trp Cys Val His Thr Ala Val Leu		
225	230	235
Leu Pro Leu Gly Gly Leu Asp Thr His Pro Ala Arg Gly Ala Thr Lys		
245	250	255
Leu Cys Pro Asp Glu Ala Arg Trp Ala Pro Arg Ser Leu Pro Leu Ser		
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Arg Gly Val Leu Ala Ser Pro Gly Phe Ala Phe Leu Arg Ile		
275	280	285

<210> B9

<211> 1023

<212> DNA

<213> Homo sapiens

<400> B9

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1023

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 <211> 149
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
 115 120 125
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 130 135 140
 Gly Tyr Leu Met Gly
 145

<210> 91
 <211> 3901
 <212> DNA
 <213> Homo sapiens

<400> 91
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 <212> PRT
 <213> Homo sapiens

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 Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
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 Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
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 Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
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 Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
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 Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
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 Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
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 Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
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 Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
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Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
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Asn Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
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<210> 93

<211> 2203

<212> DNA

<213> Homo sapiens

<400> 93

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<210> 94

<211> 674

<212> PRT

<213> Homo sapiens

<400> 94

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Ile Lys Lys Asp Pro Ala Gln Phe Leu Gln Val His Gly Arg Ala Cys
      35              40              45

Lys Val His Leu Asp Ser Ala Val Ala Leu Ala Ala Glu Ser Pro Val
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Asn Met Met Pro Trp Gln Gly Asp Thr Asn Asn Met Ile Asp Arg Phe
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Asp Val Arg Ala His Leu Asp His Ile Pro Asp Tyr Thr Pro Pro Leu
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Leu Thr Thr Ile Ser Pro Glu Gln Glu Ser Asp Glu Arg Lys Cys Asn
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Tyr Glu Arg Tyr Arg Gly Leu Val Gln Asn Asp Phe Ala Gly Ile Ser
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Glu Glu Gln Cys Leu Tyr Gln Ile Tyr Ile Asp Glu Leu Tyr Gly Gly
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Leu Gln Arg Pro Ser Glu Asp Glu Lys Lys Lys Leu Ala Glu Lys Lys
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Ala Ser Ile Gly Tyr Thr Tyr Glu Asp Ser Thr Val Ala Glu Val Glu
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Lys Ala Ala Glu Lys Pro Glu Glu Glu Glu Ser Ala Ala Glu Glu Glu
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Ser Asn Ser Asp Glu Asp Glu Val Ile Pro Asp Ile Asp Val Glu Val
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Asp Val Asp Glu Leu Asn Gln Glu Gln Val Ala Asp Leu Asn Lys Gln
      210              215              220

Ala Thr Thr Tyr Gly Met Ala Asp Gly Asp Phe Val Arg Met Leu Arg
      225              230              235              240

Lys Asp Lys Glu Glu Ala Glu Ala Ile Lys His Ala Lys Ala Leu Glu
      245              250              255

Glu Glu Lys Ala Met Tyr Ser Gly Arg Arg Ser Arg Arg Gln Arg Arg
      260              265              270

Glu Phe Arg Glu Lys Arg Leu Arg Gly Arg Lys Ile Ser Pro Pro Ser
      275              280              285

Tyr Ala Arg Arg Asp Ser Pro Thr Tyr Asp Pro Tyr Lys Arg Ser Pro
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 Thr Gly Lys Pro Pro Ala Pro Pro Gln Pro Gly Gly Pro Ala Pro Gly
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 Ala Gly Lys Glu Thr Gly Ala Ala Lys Pro Lys Leu Thr Pro Gln Glu
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 580 585 590
 Asp Lys Lys Ala Ala Gln Glu Lys Met Ile Gln Gln Glu His Glu Arg
 595 600 605
 Gln Glu Arg Glu Asp Glu Leu Arg Ala Met Ala Arg Lys Ile Arg Met
 610 615 620

Lys Glu Arg Glu Arg Arg Glu Lys Glu Arg Glu Glu Trp Glu Arg Gln
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Tyr Ser Arg Gln Ser Arg Ser Pro Ser Pro Arg Tyr Ser Arg Glu Tyr
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Arg His

<210> 95

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 95

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<210> 96

<211> 204

<212> PRT

<213> Homo sapiens

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Ser Phe Ile Lys Trp Cys Asn Ser Gly Ser Gln Glu Glu Gly Tyr Ser
 35          40          45

Gln Tyr Gln Arg Met Leu Ser Thr Leu Ser Gln Cys Glu Phe Ser Met
 50          55          60

Gly Lys Thr Leu Leu Val Tyr Asp Met Asn Leu Arg Glu Met Glu Asn
 65          70          75          80

Tyr Glu Lys Ile Tyr Lys Glu Ile Glu Cys Ser Ile Ala Gly Ala His
 85          90          95

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Glu Lys Ile Ala Glu Cys Lys Lys Gln Ile Leu Gln Ala Lys Arg Ile
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 Arg Lys Asn Arg Gln Glu Tyr Asp Ala Leu Ala Lys Val Ile Gln His
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 His Pro Asp Arg His Glu Thr Leu Lys Glu Leu Glu Ala Leu Gly Lys
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 Glu Leu Glu His Leu Ser His Ile Lys Glu Ser Val Glu Asp Lys Leu
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 <211> 955
 <212> DNA
 <213> Homo sapiens

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<210> 98
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 98
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 Asp Ile Glu Glu Lys Lys Ser Ile Lys Lys Lys Ile Lys Glu Leu Lys
 35 40 45

Phe Leu Asp Ser Lys Ile Ala Gln Asn Leu Cys Lys Tyr His Ile Pro
50 55 60

Ile Pro Phe Lys Asp Ser Gly Asn Ile Ser Leu Asn Asp Phe Ile Phe
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<210> 99

<211> 1375

<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 132

<212> PRT

<213> Homo sapiens

<400> 100

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Cys Arg Gly Ser Trp Gln Leu Leu Gly Glu Val Ser Trp His Arg Leu
35 40 45

Thr Leu Leu Ser Gly Thr Thr Ser Phe Pro Phe Glu Glu Thr Ala Thr

50

55

60

Ala Val Ala Lys Ala Ala Ala Pro Ala Met Arg Val Tyr Ile Phe
65 70 75 80

Phe Thr Gln Ser Ser Gly Ile Val His Leu Phe Phe Lys Thr Gln Arg
85 90 95

Gly Lys Gln Pro Cys Ile Ile Cys Glu His Cys Ile Ile Gly Asn Val
100 105 110

Val Gln Thr Leu Leu Tyr Ser Asp Leu Ser Cys Ser Cys Ser Lys Asn
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Pro Leu Trp Thr
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<210> 101

<211> 1213

<212> DNA

<213> Homo sapiens

<400> 101

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1213

<210> 102

<211> 108

<212> PRT

<213> Homo sapiens

<400> 102

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Cys Gly Trp Gly Val Ala Thr Thr Glu His Met Ala Val Ser Arg Arg
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Lys His Phe Ser Ser Ile Cys Leu His Ala Gln Gly Ser Ser Arg Leu
35 40 45

Pro Val Leu Ser Thr Gly Thr Ala Val Ser Glu Leu Leu Arg Thr Ser
 50 55 60

Leu Cys Gln Val Val Glu Leu Gly Pro Ser Pro Tyr Leu Ser Leu Val
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Pro Thr Val Leu Leu Thr Val Gln His Leu Gly Ala Leu Ala Trp Gly
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Trp Arg Pro Trp
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 <211> 1036
 <212> DNA
 <213> Homo sapiens

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 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 104
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 20 25 30

Tyr Glu Phe Glu Ile Thr Asp Leu Phe Ser Ser Tyr Cys Ile His Ile
 35 40 45

Asn Ile Cys Glu Phe Val Val Gln Leu Phe Ile Gln Thr Lys Asn Ile
 50 55 60

Pro Ser Arg Lys Leu His Phe Tyr His Lys His Phe Asn Ile Thr Asn
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Ile Arg Thr Ser Leu Pro Cys

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<210> 105

<211> 2349

<212> DNA

<213> Homo sapiens

<400> 105

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<210> 106

<211> 539

<212> grr

<213> Homo sapiens

<400> 106

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 Ser Ser Ser Ser Thr Asp Glu Ser Glu Asp Glu Lys Glu Glu Lys Leu
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 Thr Asp Glu Ser Arg Ser Lys Leu Tyr Asp Glu Glu Ser Leu Leu Ser
 65 70 75 80
 Leu Thr Met Ser Gln Asp Gly Phe Pro Asn Glu Asp Gly Glu Gln Met
 85 90 95
 Thr Pro Glu Leu Leu Leu Leu Gln Glu Arg Gln Arg Ala Ser Glu Trp
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 Pro Lys Asp Arg Val Leu Ile Asn Arg Ile Asp Leu Val Cys Gln Ala
 115 120 125
 Val Leu Ser Gly Lys Trp Pro Ser Ser Arg Arg Ser Gln Glu Met Val
 130 135 140
 Thr Gly Gly Ile Leu Gly Pro Gly Asn His Leu Leu Asp Ser Pro Ser
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 Leu Thr Pro Gly Glu Tyr Gly Asp Ser Pro Val Pro Thr Pro Arg Ser
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 Ala Ala Ala Gln Phe Thr Lys Leu Arg Arg Gly Met Asp Glu Lys Glu
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 Phe Thr Val Gln Ile Lys Asp Glu Glu Gly Leu Lys Leu Thr Phe Gln
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 Lys His Lys Leu Met Ala Asn Gly Val Met Gly Asp Gly His Pro Leu
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 Phe His Lys Lys Lys Gly Asn Arg Lys Lys Leu Val Glu Leu Glu Val
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 Glu Cys Met Glu Glu Pro Asn His Leu Asp Val Asp Leu Glu Thr Arg
 260 265 270
 Ile Pro Val Ile Asn Lys Val Asp Gly Thr Leu Leu Val Gly Glu Asp
 275 280 285
 Ala Pro Arg Arg Ala Glu Leu Glu Met Trp Leu Gln Gly His Pro Glu
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 Phe Ala Val Asp Pro Arg Phe Leu Ala Tyr Met Glu Asp Arg Arg Lys
 305 310 315 320
 Gln Lys Trp Gln Arg Cys Lys Lys Asn Asn Lys Ala Glu Leu Asn Cys
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Leu Gly Met Glu Pro Val Gln Thr Ala Asn Ser Arg Asn Gly Lys Lys
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 Gly His His Thr Glu Thr Val Phe Asn Arg Val Leu Pro Gly Pro Ile
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 Ala Pro Glu Ser Ser Lys Lys Arg Ala Arg Arg Met Arg Pro Asp Leu
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 Ser Lys Met Met Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser
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 Leu His Asn Thr Phe Gln His Ser Ser Ser Gly Leu Gln Ser Val Ser
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 Ser Leu Gly His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro
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 Phe Val Met Gly Gly Ala Pro Ser Ser Pro His Val Asp Ser Ser Thr
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 Met Leu His His His His His His Pro His Pro His His His His His
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 His His Pro Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr
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 Thr Ala Ser Gly Thr Thr Leu Arg Leu Pro Pro Leu Gln Pro Glu Glu
 485 490 495
 Asp Asp Asp Glu Asp Glu Glu Asp Asp Asp Asp Leu Ser Gln Gly Tyr
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<210> 107

<211> 3004

<212> DNA

<213> Homo sapiens

<400> 107

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<210> 108

<211> 959

<212> PRT

<213> Homo sapiens

<400> 108

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Leu Val Lys Glu Ala Gln Pro Leu Val Trp Val Lys Asp Pro Leu Gln
          35           40           45
Leu Thr Ser Asn Pro Leu Gly Pro Pro Glu Pro Trp Ser Ser Arg Ser
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Ser His Leu Pro Trp Glu Ser Pro His Ala Pro Ala Pro Pro Ala Ala
          65           70           75           80
Pro Gly Asp Phe Asp Tyr Leu Gly Pro Ser Ala Ser Ser Gln Met Ser

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Pro	Pro	Pro	Glu	His	Pro	Glu	Val	Thr	Leu	Pro	Pro	Ser	Asp	Lys	Gly				

	405		410		415
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Leu Glu Leu Ser Ile Thr Thr Glu Pro Thr Thr Glu Val Lys Pro Ser	435		440		445
Pro Thr Thr Glu Glu Thr Ser Ala Gln Pro Pro Asp Pro Gly Leu Ala	450		455		460
Ile Thr Pro Glu Pro Thr Thr Glu Ile Gly His Ser Thr Ala Leu Glu	465		470		475
Lys Thr Arg Ala Pro His Pro Asp Gln Val Gln Thr Leu His Arg Ser	485		490		495
Leu Thr Glu Val Thr Gly Pro Pro Thr Lys Leu Glu Ser Ser Gln Asp	500		505		510
Ser Leu Val Gln Ser Glu Thr Ala Pro Glu Glu Gln Lys Ala Ser Thr	515		520		525
Ser Thr Asn Ile Cys Glu Leu Cys Thr Cys Gly Asp Glu Thr Leu Ser	530		535		540
Cys Val Gly Leu Ser Pro Lys Gln Arg Leu Arg Gln Val Pro Val Pro	545		550		555
Glu Pro Asp Thr Tyr Asn Gly Ile Phe Thr Thr Leu Asn Phe Gln Gly	565		570		575
Asn Tyr Ile Ser Tyr Leu Asp Gly Asn Val Trp Lys Ala Tyr Ser Trp	580		585		590
Thr Glu Lys Leu Ile Leu Ser Glu Asn Tyr Leu Thr Glu Leu Pro Lys	595		600		605
Asp Ser Phe Glu Gly Leu Leu Tyr Leu Gln Tyr Leu Asp Leu Ser Cys	610		615		620
Asn Lys Ile Arg Tyr Ile Glu Arg Gln Thr Phe Glu Ser Leu Pro Phe	625		630		635
Leu Gln Tyr Ile Asn Leu Gly Cys Asn Leu Ile Thr Lys Leu Ser Leu	645		650		655
Gly Thr Phe Gln Ala Trp His Gly Met Gln Phe Leu His Asn Leu Ile	660		665		670
Leu Asn Arg Asn Pro Leu Thr Thr Val Glu Asp Pro Tyr Leu Phe Glu	675		680		685
Leu Pro Ala Leu Lys Tyr Leu Asp Met Gly Thr Thr His Ile Thr Leu	690		695		700
Thr Thr Leu Lys Asn Ile Leu Thr Met Thr Val Glu Leu Glu Lys Leu	705		710		715
Ile Leu Pro Ser His Met Ala Cys Cys Leu Cys Gln Phe Lys Asn Ser					720

725										730					735				
Ile	Glu	Ala	Val	Cys	Lys	Thr	Val	Lys	Leu	His	Cys	Asn	Thr	Ala	Cys				
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Leu	Thr	Asn	Ser	Ile	His	Cys	Pro	Glu	Glu	Ala	Ser	Val	Gly	Asn	Pro				
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Glu	Gly	Ala	Phe	Met	Lys	Met	Leu	Gln	Ala	Arg	Lys	Gln	His	Met	Ser				
770										775					780				
Thr	Gln	Leu	Thr	Ile	Glu	Ser	Glu	Ala	Pro	Ser	Asp	Ser	Ser	Gly	Ile				
785										790					795				
Asn	Leu	Ser	Gly	Phe	Gly	Gly	Asp	Gln	Leu	Glu	Ile	Gln	Leu	Thr	Glu				
805										810					815				
Gln	Leu	Arg	Ser	Leu	Ile	Pro	Asn	Glu	Asp	Val	Arg	Lys	Phe	Met	Ser				
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His	Val	Ile	Arg	Thr	Leu	Lys	Met	Glu	Cys	Ser	Glu	Thr	His	Val	Gln				
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Leu	Ser	Glu	Gln	Gln	Glu	Ala	Lys	Ala	Leu	Asn	Val	Glu	Trp	Asp	Thr				
865										870					875				
Asp	Gln	Gln	Lys	Thr	Asn	Tyr	Ile	Asn	Glu	Asn	Met	Glu	Gln	Asn	Glu				
885										890					895				
Gln	Lys	Glu	Gln	Lys	Ser	Ser	Glu	Leu	Met	Lys	Glu	Val	Pro	Gly	Asp				
900										905					910				
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915										920					925				
Ile	Ile	Leu	Ile	Ile	Ile	Phe	Cys	Leu	Ile	Glu	Val	Asn	Ser	His	Lys				
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<210> 109

<211> 1331

<212> DNA

<213> Homo sapiens

<400> 109

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1331

<210> 110

<211> 118

<212> PRT

<213> Homo sapiens

<400> 110

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Met Ile Ser Leu Tyr Gly Gln Phe Arg Val Val Ser Trp Ile Ile Thr
  1             5             10             15

```

```

Ile Trp Ile Phe Gly Ser Leu Thr Ile Phe Leu Leu Ala Arg Val Leu
          20             25             30

```

```

Gly Gly Glu Val Ala Tyr Gly Gln Val Leu Gly Val Ile Gly Tyr Ser
          35             40             45

```

```

Leu Leu Pro Leu Ile Val Ile Ala Pro Val Leu Leu Val Val Gly Ser
          50             55             60

```

```

Phe Glu Val Val Ser Thr Leu Ile Lys Leu Phe Gly Val Phe Trp Ala
          65             70             75             80

```

```

Ala Tyr Ser Ala Ala Ser Leu Leu Val Gly Glu Glu Phe Lys Thr Lys
          85             90             95

```

```

Lys Pro Leu Leu Ile Tyr Pro Ile Phe Leu Leu Tyr Ile Tyr Phe Leu
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```

```

Ser Leu Tyr Thr Gly Val
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```

<210> 111

<211> 2610

<212> DNA

<213> Homo sapiens

<400> 111

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<210> 112
 <211> 116
 <222> PRT
 <213> Homo sapiens

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<400> 112
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Leu Ser Leu Tyr Thr His Val Thr Cys Ser Ser Leu Pro Ser Ser Leu
  20             25             30

Cys Leu Tyr Ile Tyr Tyr Tyr His Arg Gly Leu Gly Lys Lys Thr Pro
  35             40             45

Thr Ala Ala Pro His Thr His Pro Pro Ala Leu Tyr His Leu Leu Cys
  50             55             60

Phe Val Phe Leu Cys Arg Ile His Asp Phe Leu Lys Tyr Asn Phe Phe
  65             70             75             80

Asn Val Tyr Ile Leu Tyr Ala Phe Ser His Ser Tyr Val Lys Ser Gly
  85             90             95

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Arg His Arg Leu Val Phe Leu Phe Thr Val Asp Ala Ser Val Pro Lys
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Ile Cys Ile Ala
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<210> 113
<211> 2759
<212> DNA
<213> Homo sapiens

<400> 113

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<210> 114
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Ala Glu Gly Gly Phe Asp Pro Cys Glu Cys Val Cys Ser His Glu
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 20 25 30
 Cys Thr Asp Thr Glu Cys Leu Gln Gly Leu Pro Gly Pro Ser Gly Asp
 35 40 45
 Asn Gly Ile Ser Val Thr Met Ile Leu Val Ala Trp Met Val Ile Ala
 50 55 60
 Leu Ile Leu Phe Leu Leu Arg Pro Pro Asn Leu Arg Gly Ser Ser Leu
 65 70 75 80
 Pro Gly Lys Pro Thr Ser Pro His Asn Gly Gln Asp Pro Pro Ala Pro
 85 90 95
 Pro Val Asp

<210> 115
 <211> 1404
 <212> DNA
 <213> Homo sapiens

<400> 115
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<210> 116
 <211> 184
 <212> PRP
 <213> Homo sapiens

<400> 116

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Ser Ala Leu Thr Pro Leu Trp Ser Pro Tyr Pro Ala Gly Phe Leu Leu
      20               25               30

Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu
      35               40               45

Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu
      50               55               60

Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu
      65               70               75               80

Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val
      85               90               95

Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu
     100               105               110

Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser
     115               120               125

His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys
     130               135               140

Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser
     145               150               155               160

Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly
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Leu Ala Leu Glu Ile Arg Ser Leu
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<210> 117
 <211> 1802
 <212> DNA
 <213> Homo sapiens

<400> 117

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<210> 119

<211> 86

<212> PRT

<213> Homo sapiens

<400> 118

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Met Val Arg Lys Val Asn Ala His Leu Pro Leu Ser Phe Pro Thr Val
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Glu Thr Asp Ser Arg Glu Ile Leu Gln Val Arg Cys Tyr Val Gly Leu
      20             25             30

Arg Glu Arg Cys Tyr Asp Gln Thr Glu Pro Phe Ser Leu Pro Ser Val
      35             40             45

His Gly Phe Ser Trp Leu Cys Gly Pro Val Ser Cys His Ser Phe Thr
      50             55             60

Pro Asn Phe Trp Asp Ile Gln Gly Asn Asn Leu Ala Thr Gly Tyr Leu
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Leu Val Glu Ile Met Trp
              85

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<213> Homo sapiens

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Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr
      20              25              30

Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu
      35              40              45

Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu
      50              55              60

Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys
      65              70              75              80

Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val
      85              90              95

Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu
      100             105             110

Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu
      115             120             125

Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His
      130             135             140

Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro
      145             150             155             160

Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys
      165             170             175

Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly
      180             185             190

His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe
      195             200             205

Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val
      210             215             220

Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys
      225             230             235             240

Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln
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Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr
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 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe
 290 295 300
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp
 305 310 315 320
 Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn
 325 330 335
 Thr Lys Val Ala Lys Leu Thr Asn Glu Leu Lys Glu Glu Gln Glu Met
 340 345 350
 Asn Lys Cys Leu Arg Ala Asn Gln Val Leu Leu Gln Asn Lys Leu Lys
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 Glu Glu Glu Arg Val Leu Lys Glu Thr Cys Asp Gln Lys Asp Leu Gln
 370 375 380
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<213> Homo sapiens

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 35 40 45
 Leu Gly Phe Phe Val Gly Leu Ile Pro His Leu Leu Gly Asp Val Val
 50 55 60
 Phe Leu Trp Gly Cys Asn Leu Leu Ala His Phe Ile Asn Ala Tyr Leu
 65 70 75 80
 Val Asp Asp Ser Phe Ser Gln Ala Leu Ala Ile Arg Ser Tyr Thr Lys
 85 90 95
 Phe Val Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu
 100 105 110
 Val Gly Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu
 115 120 125
 Pro Pro Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr
 130 135 140
 Leu Ser Val Gln Gly Gln Leu Phe Arg Gly Ser Ser Leu Leu Phe Arg

145 150 155 160
 Arg Val Ser Ser Gly Ser Cys Phe Ala Leu Glu
 165 170

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 Glu Leu Leu Leu Leu Leu Leu His Leu Gln Trp Gly Leu Gly Leu Leu
 35 40 45
 Arg Gln Leu His His Lys Arg Leu Ala Gln Leu Leu Leu His Arg Arg
 50 55 60
 Arg Asp His Pro Ile Pro Pro Ile Gln Asp Ile Leu Gly Ile Ala Lys
 65 70 75 80
 Cys Pro Cys Pro Trp Ala Ile Ile Leu Met Arg Met Ala Ser Ile Ile
 85 90 95
 Cys His Ile His Gln Cys Ile Thr Arg Val Leu Asp Arg Leu His Thr
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 130 135 140

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 His Leu Leu Pro Cys Ser Val Ser Ser Leu Ser Pro Arg Leu Ala Gln
 35 40 45
 Glu Cys Trp Lys Ser Ser Arg Leu Gly Leu Gly Ala Trp Pro Leu Asp
 50 55 60
 Ile Pro Arg Ala Ser Pro Val Leu Pro Ser Pro Arg Thr Thr Gly Pro
 65 70 75 80

WO 99/57132

PCT/US99/09970

Leu Ala

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